

SEQUENCE LISTING

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Bachmann, Martin  
Tissot, Alain  
Maurer, Patrick  
Lechner, Franziska  
Sebbel, Peter  
Piossek, Christine

<120> Molecular Antigen Array

<130> 1700.0190004

<140> (To be assigned)

<141> 2002-01-18

<150> US 60/262,379

<151> 2001-01-19

<150> US 60/288,549

<151> 2001-05-04

<150> US 60/326,998

<151> 2001-10-05

<150> US 60/331,045

<151> 2001-11-07

<160> 350

<170> PatentIn Ver. 2.1

<210> 1

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<220>

<223> Description of Artificial Sequence: Primer

<400> 1

ggggacgcgt gcagcaggta accaccgtta aagaaggcac c

41

<210> 2

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2

cgggtggttac ctgctgcacg cggttgcttaa gcgacatgta gcgg

44

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 3  
 ccatgaggcc tacgataccc 20

<210> 4  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 4  
 ggcactcacg gcgcgcttta caggc 25

<210> 5  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 5  
 ctttctttaa cggctggttac ctgctggcaa ccaacgtggt tcatgac 47

<210> 6  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 6  
 aagcatgctg cacgcgtgtg cggtggctcg atcgcccggc 40

<210> 7  
 <211> 90  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 gggcttagat tccaaccat tcccttatcc aggctttttg acaacgctat gctccgcgcc 60  
 catcgtctgc accagctggc ctttgacacc 90

<210> 8  
 <211> 108  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

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<400> 8  
gggtctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60  
gctggtttcg ctaccgtagc gcaggccttc ccaaccattc cttatcc 108

<210> 9  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 9  
cccgaattcc tagaagccac agctgccctc c 31

<210> 10  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 10  
cctgcggtgg tctgaccgac accc 24

<210> 11  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g 41

<210> 12  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
ctatcatcta gaatgaatag aggattcttt aac 33

<210> 13  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Modified ribosome  
binding site

100505002-01300

<400> 13  
aggaggtaaa aaacg

15

<210> 14  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: signal peptide

<400> 14  
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
1 5 10 15  
Thr Val Ala Gln Ala  
20

<210> 15  
<211> 46  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified Fos  
construct

<400> 15  
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu  
1 5 10 15  
Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu  
20 25 30  
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys  
35 40 45

<210> 16  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide linker

<400> 16  
Ala Ala Ala Ser Gly Gly  
1 5

<210> 17  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide linker

<400> 17  
Gly Gly Ser Ala Ala Ala

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1

5

<210> 18  
<211> 256  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fos fusion construct

<400> 18  
gaattcagga ggtaaaaaaac gatgaaaaaag acagctatcg cgattgcagt ggcaactggct 60  
ggtttcgcta ccgtagcgca ggcctgggtg ggggcggccg cttctgggtg ttgcgggtggt 120  
ctgaccgaca ccctgcaggc ggaaaccgac caggtggaag acgaaaaatc cgcgctgcaa 180  
accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240  
ggtggttgct aagctt 256

<210> 19  
<211> 52  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fos fusion construct

<400> 19  
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala  
5 10 15  
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile  
20 25 30  
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala  
35 40 45  
His Gly Gly Cys  
50

<210> 20  
<211> 261  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fos fusion  
construct

<220>  
<221> CDS  
<222> (22)..(240)

<400> 20  
gaattcagga ggtaaaaaaac g atg aaa aag aca gct atc gcg att gca gtg 51  
Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
1 5 10  
gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc 99  
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr  
15 20 25

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gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg 147  
 Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala  
                   30                  35                  40

ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag 195  
 Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu  
                   45                  50                  55

ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct 240  
 Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala  
           60                  65                  70

gggtgtgggg atatcaagct t 261

<210> 21  
 <211> 73  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
 construct

<400> 21  
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
   1                  5                  10                  15

Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu  
           20                  25                  30

Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala  
           35                  40                  45

Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His  
   50                  55                  60

Gly Gly Cys Gly Gly Ser Ala Ala Ala  
   65                  70

<210> 22  
 <211> 196  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
 construct

<220>  
 <221> CDS  
 <222> (34)..(189)

<400> 22  
 gaattcagga ggtaaaaaga tatcgggtgt ggg gcg gcc gct tct ggt ggt tgc 54  
                                   Ala Ala Ala Ser Gly Gly Cys  
                                   1                  5

ggt ggt ctg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac 102  
 Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp  
           10                  15                  20

20050500E 0130E

gaa aaa tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa 150  
 Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys  
           25                          30                          35

gaa aag ctg gag ttc atc ctg gcg gca cac ggt ggt tgc taagctt 196  
 Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys  
           40                          45                          50

<210> 23  
 <211> 52  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
           construct

<400> 23  
 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala  
       1                          5                          10                          15  
 Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile  
                           20                          25                          30  
 Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala  
                           35                          40                          45  
 His Gly Gly Cys  
           50

<210> 24  
 <211> 204  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
           construct

<400> 24  
 gaattcagga ggtaaaaaac gatggcttgc ggtggtctga ccgacaccct gcaggcggaa 60  
 accgaccagg tggaagacga aaaatccgcy ctgcaaaccg aaatcgcgaa cctgctgaaa 120  
 gaaaaagaaa agctggagtt catcctggcg gcacacggtg gttgcggttg ttctgcggcc 180  
 gctgggtgtg gggatatcaa gctt 204

<210> 25  
 <211> 56  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
           construct

<400> 25  
 Lys Thr Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr  
       1                          5                          10                          15  
 Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn

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Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly  
 20 25 30  
 35 40 45  
 Gly Cys Gly Gly Ser Ala Ala Ala  
 50 55

<210> 26  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu  
 1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala  
 20 25

<210> 27  
 <211> 262  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
 construct

<400> 27  
 gaattcaggc ctatggctac aggcctcccg acgtccctgc tcctggcttt tggcctgctc 60  
 tgcctgccct ggcttcaaga gggcagcgct ggggtgtggg cggccgcttc tgggtggtgc 120  
 ggtggtctga ccgacaccct gcaggcggaa accgaccagg tggaagacga aaaatccgcg 180  
 ctgcaaaccg aaatcgcgaa cctgctgaaa gaaaaagaaa agctggagtt catcctggcg 240  
 gcacacggtg gttgctaagc tt 262

<210> 28  
 <211> 52  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fos fusion  
 construct

<400> 28  
 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala  
 5 10 15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile  
 20 25 30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala  
 35 40 45

His Gly Gly Cys  
 50

<210> 29

10050900.04300



<211> 261  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fos fusion  
construct

<220>  
<221> CDS  
<222> (7)..(240)

<400> 29  
gaattc atg gct aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc 48  
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly  
1 5 10  
ctg ctc tgc ctg ccc tgg ctt caa gag ggc agc gct tgc ggt ggt ctg 96  
Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu  
15 20 25 30  
acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc 144  
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser  
35 40 45  
gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg 192  
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu  
50 55 60  
gag ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct 240  
Glu Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala  
65 70 75  
gggtgtggga ggcctaagct t 261

<210> 30  
<211> 78  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fos fusion  
construct

<400> 30  
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu  
1 5 10 15  
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu Thr Asp  
20 25 30  
Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu  
35 40 45  
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe  
50 55 60  
Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala  
65 70 75

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<210> 31  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 31  
cctgggtggg ggcggccgct tctggtggtt gcggtggtct gacc 44

<210> 32  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 32  
ggtgggaatt caggaggtaa aaagatatcg ggtgtggggc ggcc 44

<210> 33  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 33  
ggtgggaatt caggaggtaa aaaacgatgg cttgcggtgg tctgacc 47

<210> 34  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 34  
gcttgcggtg gtctgacc 18

<210> 35  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 35  
ccaccaagct tagcaaccac cgtgtgc 27

<210> 36  
<211> 54  
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

ccaccaagct tgatatcccc acaccagcg gccgcagaac caccgcaacc accg

54

<210> 37

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

ccaccaagct taggcctccc acaccagcg gc

32

<210> 38

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38

ggtgggaatt caggaggtaa aaaacgatg

29

<210> 39

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39

ggtgggaatt caggcctatg gctacaggct cc

32

<210> 40

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

ggtgggaatt catggctaca ggctccc

27

<210> 41

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Primer

<400> 41  
gggtctagaa tggctacagg ctcccgagc tccctgctcc tggcttttgg cctgctctg 59

<210> 42  
<211> 58  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 42  
cgcaggcctc ggcactgccc tcttgaagcc agggcaggca gagcaggcca aaagccag 58

<210> 43  
<211> 402  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Modified bee  
venom phospholipase A2

<220>  
<221> CDS  
<222> (1)..(402)

<400> 43  
atc atc tac cca ggt act ctg tgg tgt ggt cac ggc aac aaa tct tct 48  
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser  
1 5 10 15  
ggt ccg aac gaa ctc ggc cgc ttt aaa cac acc gac gca tgc tgt cgc 96  
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg  
20 25 30  
acc cag gac atg tgt ccg gac gtc atg tct gct ggt gaa tct aaa cac 144  
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His  
35 40 45  
ggg tta act aac acc gct tct cac acg cgt ctc agc tgc gac tgc gac 192  
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp  
50 55 60  
gac aaa ttc tac gac tgc ctt aag aac tcc gcc gat acc atc tct tct 240  
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser  
65 70 75 80  
tac ttc gtt ggt aaa atg tat ttc aac ctg atc gat acc aaa tgt tac 288  
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr  
85 90 95  
aaa ctg gaa cac ccg gta acc ggc tgc ggc gaa cgt acc gaa ggt cgc 336  
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg  
100 105 110  
tgc ctg cac tac acc gtt gac aaa tct aaa ccg aaa gtt tac cag tgg 384  
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp  
115 120 125

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ttc gac ctg cgc aaa tac  
Phe Asp Leu Arg Lys Tyr  
130

402

<210> 44  
<211> 134  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Modified bee  
venom phospholipase A2

<400> 44  
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser  
1 5 10 15  
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg  
20 25 30  
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His  
35 40 45  
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp  
50 55 60  
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser  
65 70 75 80  
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr  
85 90 95  
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg  
100 105 110  
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp  
115 120 125  
Phe Asp Leu Arg Lys Tyr  
130

<210> 45  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 45  
ccatcatcta cccaggtac

19

<210> 46  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Primer

<400> 46  
cccacacca gcggccgcgt atttgcgag gtcg 34

<210> 47  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 47  
cgggtggttct gcggccgcta tcattctacc aggtac 36

<210> 48  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 48  
ttagtatttg cgcaggtcg 19

<210> 49  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 49  
ccggctccat cggtagcag 18

<210> 50  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 50  
accaccagaa gcggccgcag gggaaacaca tctgcc 36

<210> 51  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 51

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cggtggttct gcggccgctg gctccatcgg tgcag 35

<210> 52  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 52  
ttaaggggaa acacatctgc c 21

<210> 53  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 53  
actagtctag aatgagagtg aaggagaaat atc 33

<210> 54  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 54  
tagcatgcta gcaccgaatt tatctaattc caataattct tg 42

<210> 55  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 55  
gtagcaccca ccaaggcaaa gctgaaagct acccagctcg agaaactggc a 51

<210> 56  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 56  
caaagctcct attcccactg ccagtttctc gagctgggta gctttcag 48

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<210> 57  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 57  
ttcgggtgcta gcggtggctg cgggtggtctg accgac 36

<210> 58  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 58  
gatgctgggc ccttaaccgc aaccaccgtg tgccgcc 37

<210> 59  
<211> 46  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: JUN amino acid  
sequence

<400> 59  
Cys Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys  
1 5 10 15  
Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln  
20 25 30  
Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Gly Cys  
35 40 45

<210> 60  
<211> 46  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FOS amino  
acid sequence

<400> 60  
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu  
1 5 10 15  
Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu  
20 25 30  
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys  
35 40 45

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<210> 61  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 61  
ccggaattca tgtgcggtgg tcggatcgcc cgg 33

<210> 62  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 62  
gtcgcgtaccc gcggctccgc aaccaacgtg gtcatgac 39

<210> 63  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 63  
gttggttgcg gagccgcggg tagcgacatt gacccttata aagaatttgg 50

<210> 64  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 64  
cgcgtcccaa gcttctacgg aagcgttgat aggatagg 38

<210> 65  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 65  
ctagccgcgg gttgcggtgg tcggatcgcc cgg 33

<210> 66  
<211> 38  
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 66

cgcggtcccaa gcttttagca accaacgtgg ttcattgac

38

<210> 67

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 67

ccggaattca tggacattga cccttataaa g

31

<210> 68

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 68

ccgaccaccg caaccgcggg ctagcggaag cggtgatagg atagg

45

<210> 69

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 69

ctaattgatc cggtgggggc tgcggtgggc ggatcgcccg gctcgag

47

<210> 70

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 70

gtcgctaccc ggcgctccgc aaccaacgtg gttcatgac

39

<210> 71

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Primer

<400> 71  
ccggaattca tggacattga cccttataaa g 31

<210> 72  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 72  
ccgaccaccg cagccccac cggatccatt agtaccacc caggtagc 48

<210> 73  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 73  
gttggttgcg gagccgcggg tagcgaccta gtagtcagtt atgtc 45

<210> 74  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 74  
cgcgccccaa gcttctacgg aagcggtgat aggatagg 38

<210> 75  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 75  
ctagccgcgg gttgcggtgg tcggatcgcc cgg 33

<210> 76  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 76

10050902.01302

cgcggtcccaa gcttttagca accaacgtgg ttcattgac

38

<210> 77  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 77  
ccggaattca tggccacact tttaaggagc

30

<210> 78  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 78  
cgcggtcccaa gcttttagca accaacgtgg ttcattgac

38

<210> 79  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 79  
ccggaattca tggacattga cccttataaa g

31

<210> 80  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 80  
cctagagcca cctttgccac catcttctaa attagtagcc acccaggtag c

51

<210> 81  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 81  
gaagatgggtg gcaaagggtgg ctctagggac ctagtagtca gttatgtc

48

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<210> 82  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 82  
cgcggtcccaa gcttctaaac aacagtagtc tccggaag 38

<210> 83  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 83  
gccgaattcc tagcagctag caccgaattt atctaa 36

<210> 84  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 84  
ggttaagtcg acatgagagt gaaggagaaa tat 33

<210> 85  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 85  
taaccgaatt caggaggtaa aaagatatgg 30

<210> 86  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 86  
gaagtaaagc ttttaaccac cgcaaccacc agaag 35

<210> 87  
<211> 33  
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 87

tcgaatgggc cctcatcttc gtgtgctagt cag

33

<210> 88

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fos fusion construct

<400> 88

Glu Phe Arg Arg  
1

<210> 89

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 89

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Gly Ser Gln Cys

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180

<210> 90  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 90  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr  
 65 70 75 80  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
 85 90 95  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Thr Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Cys Val Ile Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 145 150 155 160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175  
 Gln Ser Arg Gly Ser Gln Cys  
 180

<210> 91  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 91  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60

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Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 92

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 92

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

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Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 93  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 93  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Thr Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
 65 70 75 80  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
 85 90 95  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 145 150 155 160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175  
 Gln Ser Arg Glu Ser Gln Cys  
 180

<210> 94  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

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<400> 94

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 95

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 95

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60

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Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 96  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 96  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro Gln  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

208T9"2060500T

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 97  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 97  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Lys Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Gly Ser Gln Cys  
210

208TTD"2060500T

<210> 98  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 98  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ala  
 65 70 75 80  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
 85 90 95  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Asp Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Ser Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 145 150 155 160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175  
 Gln Ser Arg Glu Ser Gln Cys  
 180

<210> 99  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 99  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60

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Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Glu Ser Gln Cys  
180

<210> 100  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 100  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

10050902 . 011802

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 101  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 101  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 102  
<211> 183  
<212> PRT

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic human Hepatitis B construct

<400> 102

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Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
           20           25           30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
           35           40           45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
           50           55           60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
           65           70           75           80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
           85           90           95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
           100           105           110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
           115           120           125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
           130           135           140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
           145           150           155           160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
           165           170           175

Gln Ser Arg Glu Ser Gln Cys
           180

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<210> 103

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 103

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Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1           5           10           15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
           20           25           30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
           35           40           45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
           50           55           60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
           65           70           75           80

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His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Ser  
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 104  
<211> 183  
<212> PRT  
<213> Hepatitis B virus

<400> 104  
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

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Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Glu Ser Gln Cys  
180

<210> 105

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 105

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Glu Ser Gln Cys  
180

<210> 106

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 106

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys

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35	40	45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu		
50	55	60
Leu Met Thr Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala		
65	70	75
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys		
	85	90
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg		
	100	105
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr		
	115	120
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro		
	130	135
Glu Thr Thr Val Val Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr		
145	150	155
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser		
	165	170
Gln Ser Arg Glu Ser Gln Cys		
	180	

<210> 107

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 107

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

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Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 108  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 108  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

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<210> 109  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 109  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ala Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 110  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 110  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30

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Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Phe Glu Cys Ser Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 111  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<220>  
<221> UNSURE  
<222> (28)  
<223> May be any amino acid.

<400> 111  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

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His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr  
85 90 95

Leu Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Thr Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 112  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 112  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

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Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 113  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 113  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 114

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<211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 114  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Pro Gln Cys  
 210

<210> 115  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 115  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45

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Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Ser Thr Ala Ser  
50 55 60  
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80  
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95  
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110  
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125  
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140  
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160  
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175  
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190  
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205  
Glu Ser Gln Cys  
210

<210> 116  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 116  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15  
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30  
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45  
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60  
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80  
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95  
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110  
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

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Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Leu Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 117  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 117  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Lys Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205

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Glu Ser Gln Cys  
210

<210> 118  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 118  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15  
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30  
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45  
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala  
50 55 60  
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80  
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95  
Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110  
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125  
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140  
Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160  
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175  
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190  
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205  
Glu Ser Gln Cys  
210

<210> 119  
<211> 183  
<212> PRT  
<213> Hepatitis B virus

<400> 119  
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Met Glu Leu Leu  
1 5 10 15

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Ser Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Thr Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Gln Asp Pro Thr  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Val Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Val Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Gln Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Glu Ser Gln Cys  
180

<210> 120  
<211> 183  
<212> PRT  
<213> Hepatitis B virus

<400> 120  
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

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Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 145 150 155 160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175  
 Gln Ser Arg Glu Ser Gln Cys  
 180

<210> 121  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 121  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 122

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<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 122  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15  
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30  
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45  
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60  
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80  
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95  
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110  
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125  
Leu Leu Trp Phe His Ile Ser Cys Leu Ile Phe Gly Arg Glu Thr Val  
130 135 140  
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160  
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175  
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190  
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205  
Glu Ser Gln Cys  
210

<210> 123  
<211> 183  
<212> PRT  
<213> Hepatitis B virus

<400> 123  
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15  
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30  
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

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Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Val  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

Pro Ser Pro Ala Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Glu Ser Gln Cys  
180

<210> 124  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 124  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Asn  
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp  
100 105 110

Leu Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

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Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 125  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 125  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
 65 70 75 80  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
 85 90 95  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr  
 145 150 155 160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175  
 Gln Ser Arg Glu Ser Gln Cys  
 180

<210> 126  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 126  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

30050900-011803

1	5	10	15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile	20	25	30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu	35	40	45
Pro Ser Asp Phe Phe Pro Ser Val Arg Ala Leu Leu Asp Thr Ala Ser	50	55	60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His	65	70	75
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr	85	90	95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp	100	105	110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln	115	120	125
Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val	130	135	140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala	145	150	155
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr	165	170	175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro	180	185	190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg	195	200	205
Glu Ser Gln Cys	210		

<210> 127  
 <211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 127

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr	1	5	10	15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile	20	25	30	
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu	35	40	45	
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser	50	55	60	
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His	65	70	75	80

10050902-011802

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Thr Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205

Glu Ser Gln Cys  
210

<210> 128  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 128  
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160

10050902-01802

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175  
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190  
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Thr Arg Ser Gln Ser Arg  
195 200 205  
Glu Ser Gln Cys  
210

<210> 129  
<211> 212  
<212> PRT  
<213> Hepatitis B virus

<400> 129  
Met Gln Leu Phe His Leu Cys Leu Val Ile Ser Cys Ser Cys Pro Thr  
1 5 10 15  
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
20 25 30  
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
35 40 45  
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala  
50 55 60  
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
65 70 75 80  
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr  
85 90 95  
Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp  
100 105 110  
Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln  
115 120 125  
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
130 135 140  
Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
145 150 155 160  
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
165 170 175  
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
180 185 190  
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
195 200 205  
Glu Ser Gln Cys  
210

<210> 130

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<211> 212  
 <212> PRT  
 <213> Hepatitis B virus

<400> 130  
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Ala Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr  
 85 90 95  
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp  
 100 105 110  
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln  
 115 120 125  
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Cys  
 210

<210> 131  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 131  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45

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Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala  
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Glu Ser Gln Cys  
180

<210> 132  
<211> 183  
<212> PRT  
<213> Hepatitis B virus

<400> 132  
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile  
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
145 150 155 160

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20870" 2065001

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
165 170 175

Gln Ser Arg Gly Ser Gln Cys  
180

<210> 133  
<211> 3221  
<212> DNA  
<213> Hepatitis B virus

<220>  
<221> CDS  
<222> (1901)..(2458)

<400> 133  
ttccactgcc ttccaccaag ctctgcagga cccagagtc aggggtctgt attttctctgc 60  
tggtggctcc agttcaggaa cagtaaacc tgcctccgaat attgcctctc acatctcgtc 120  
aatctccgcg aggactgggg accctgtgac gaacatggag aacatcacat caggattcct 180  
aggacccctg ctctgtgttac aggcgggggtt tttattgttg acaagaatcc tcacaatacc 240  
gcagagtcta gactcgtggg ggacttctct caattttata gggggatcac ccgtgtgtct 300  
tggccaaaat tcgcagtcct caacctccaa tcaactacca acctcctgtc ctccaatttg 360  
tcctgggttat cgctggatgt gtctgaggcg ttttatcata ttctcttca tcctgctgct 420  
atgcctcatc ttcttattgg ttcttctgga ttatcaaggt atgttgcccg tttgtcctct 480  
aattccagga tcaacaacaa ccagtacggg accatgcaaa acctgcacga ctctgctca 540  
aggcaactct atgtttccct catgttgctg tacaaaacct acggttgga attgcacctg 600  
tattcccatc ccctcgtcct gggctttcgc aaaataccta tgggagtggg cctcagtcctg 660  
tttctcttgg ctcatgttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac 720  
tgtttggtct tcagctatat ggatgatgtg gtattggggg ccaagtctgt acagcatcgt 780  
gagtcctttt ataccgctgt taccaatttt cttttgtctc tgggtataca tttaaaccct 840  
aacaaaacaa aaagatgggg ttattcccta aacttcatgg gttacataat tggaagtgg 900  
ggaacattgc cacaggatca tattgtacaa aagatcaaac actgttttag aaaacttcct 960  
gttaacaggc ctattgattg gaaagtatgt caaagaattg tgggtctttt gggctttgct 1020  
gctccattta cacaatgtgg atatcctgcc ttaatgcctt tgtatgcatg tatacaggct 1080  
aaacaggctt tcaactttct gccaaactac aaggcctttc taagtaaaca gtacatgaac 1140  
ctttaccccg ttgctcggca acggcctggg ctgtgccaaag tgtttgctga cgcaaccccc 1200  
actggttggg gcttggccat aggccatcag cgcagtgtg gaacctttgt ggctcctctg 1260  
ccgatccata ctgcggaact cctagccgct tgtattgtct gcagccgggc tggagcaaag 1320  
ctcatcgga ctgacaattc tgctgtcctc tcgcggaaat atacatcgtt tccatggctg 1380

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ctaggctgta ctgccaactg gatccttcgc gggacgtcct ttgtttacgt cccgtcggcg 1440  
ctgaatcccg cggacgaccc ctctcggggc cgcttggggac tctatcgtcc ccttctccgt 1500  
ctgccgttcc agccgaccac ggggcgaccc tctctttacg cggctctccc gtctgtgcct 1560  
tctcatctgc cggctccgtgt gcacttcgct tcacctctgc acgttgcatg gagaccaccg 1620  
tgaacgcca tcagatcctg cccaaggtct tacataagag gactcttgga ctcccagcaa 1680  
tgtcaacgac cgaccttgag gcctacttca aagactgtgt gtttaaggac tgggaggagc 1740  
tgggggagga gattaggtta aaggctcttg tattaggagg ctgtaggcat aaattgggtct 1800  
gcgcaccagc accatgcaac tttttcacct ctgcctaata atctcttgta catgtccac 1860  
tggtcaagcc tccaagctgt gccttgggtg gctttggggc atg gac att gac cct 1915  
Met Asp Ile Asp Pro  
1 5  
tat aaa gaa ttt gga gct act gtg gag tta ctc tcg ttt ttg cct tct 1963  
Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser  
10 15 20  
gac ttc ttt cct tcc gtc aga gat ctc cta gac acc gcc tca gct ctg 2011  
Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu  
25 30 35  
tat cga gaa gcc tta gag tct cct gag cat tgc tca cct cac cat act 2059  
Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr  
40 45 50  
gca ctc agg caa gcc att ctc tgc tgg ggg gaa ttg atg act cta gct 2107  
Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala  
55 60 65  
acc tgg gtg ggt aat aat ttg gaa gat cca gca tcc agg gat cta gta 2155  
Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val  
70 75 80 85  
gtc aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg 2203  
Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu  
90 95 100  
tgg ttt cat ata tct tgc ctt act ttt gga aga gag act gta ctt gaa 2251  
Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu  
105 110 115  
tat ttg gtc tct ttc gga gtg tgg att cgc act cct cca gcc tat aga 2299  
Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg  
120 125 130  
cca cca aat gcc cct atc tta tca aca ctt ccg gaa act act gtt gtt 2347  
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val  
135 140 145  
aga cga cgg gac cga ggc agg tcc cct aga aga aga act ccc tcg cct 2395  
Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
150 155 160 165  
cgc aga cgc aga tct caa tcg ccg cgt cgc aga aga tct caa tct cgg 2443  
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
170 175 180

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gaa tct caa tgt tag tattccttgg actcataagg tgggaaaactt tactgggctt 2498  
 Glu Ser Gln Cys  
 185

tattcctcta cagtacctat cttaaatcct gaatggcaaa ctccttcctt tcctaagatt 2558

catttacaag aggacattat tgataggtgt caacaatttg tggggcctct cactgtaaatt 2618

gaaaagagaa gattgaaatt aattatgcct gctagattct atcctaccca cactaaatat 2678

ttgcccttag acaaaggaat taaaccttat tatccagatc aggtagttaa tcattacttc 2738  
 caaaccagac attattttaca tactcttttg aaggctggta ttctatataa gagggaaacc 2798

acacgtagcg catcattttg cgggtcacca tattcttggg aacaagagct acagcatggg 2858

aggttgggtca ttaaaacctc gcaaaggcat ggggacgaat ctttctgttc ccaaccctct 2918

gggattcttt cccgatcatc agttggaccc tgcattcgga gccaaactcaa acaatccaga 2978

ttgggacttc aaccccatca aggaccactg gccagcagcc aaccaggtag gagtgggagc 3038

attcgggcca gggctcacc ctccacacgg cgggtattttg ggggtggagcc ctcaggctca 3098

gggcatattg accacagtgt caacaattcc tctcctgcc tccaccaatc ggcagtcagg 3158

aaggcagcct actcccatct ctccacctct aagagacagt catcctcagg ccatgcagtg 3218

gaa 3221

<210> 134  
 <211> 185  
 <212> PRT  
 <213> Hepatitis B virus

<400> 134  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala  
 65 70 75 80  
 Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys  
 85 90 95  
 Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg  
 145 150 155 160  
 Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg  
 165 170 175  
 Arg Ser Gln Ser Arg Glu Ser Gln Cys  
 180 185

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<210> 135  
 <211> 188  
 <212> PRT  
 <213> Woodchuck hepatitis B virus

<400> 135  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu  
 1 5 10 15  
 Asn Phe Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp  
 20 25 30  
 Thr Ala Thr Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu  
 50 55 60  
 Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln  
 65 70 75 80  
 Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys  
 85 90 95  
 Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln  
 100 105 110  
 His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser  
 145 150 155 160  
 Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro  
 165 170 175  
 Arg Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys  
 180 185

<210> 136  
 <211> 217  
 <212> PRT  
 <213> Ground squirrel hepatitis virus

<400> 136  
 Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro  
 1 5 10 15  
 Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp  
 20 25 30  
 Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe  
 35 40 45  
 Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala  
 50 55 60  
 Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro  
 65 70 75 80

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His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr  
85 90 95  
Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg  
100 105 110  
Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln  
115 120 125  
Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val  
130 135 140  
Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro  
145 150 155 160  
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr  
165 170 175  
Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg  
180 185 190  
Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg  
195 200 205  
Arg Ser Gln Ser Pro Ala Ser Asn Cys  
210 215

<210> 137  
<211> 262  
<212> PRT  
<213> Snow Goose Hepatitis B Virus

<400> 137  
Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro  
1 5 10 15  
Asp Asp Phe Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp  
20 25 30  
Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu  
35 40 45  
Ile Ala Thr His Phe Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr  
50 55 60  
Gln Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro  
65 70 75 80  
Thr Thr Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala  
85 90 95  
Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile  
100 105 110  
Val Ser Phe Gln Pro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His  
115 120 125  
Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg  
130 135 140  
Arg Leu Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr  
145 150 155 160

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Val Thr Asn Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu  
165 170 175

Lys Tyr Arg Gly Arg Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro  
180 185 190

Ile Gln Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys  
195 200 205

Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val  
210 215 220

Tyr Gly Arg Arg Arg Ser Lys Ser Arg Glu Arg Arg Ala Ser Ser Pro  
225 230 235 240

Gln Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser Ser His His Arg  
245 250 255

Ser Pro Ser Pro Arg Lys  
260

<210> 138  
<211> 305  
<212> PRT  
<213> Duck hepatitis B virus

<400> 138  
Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln  
1 5 10 15

Gly Ile Phe Thr Ser Ser Leu Leu Leu Phe Leu Val Thr Val Pro Leu  
20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala  
35 40 45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro  
50 55 60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr  
65 70 75 80

Trp Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe  
85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu  
100 105 110

Ile Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val  
115 120 125

Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu  
130 135 140

Gly Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Pro  
145 150 155 160

Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala  
165 170 175

Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp  
180 185 190

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His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile  
195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys  
210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln  
225 230 235 240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu  
245 250 255

Pro Arg Arg Arg Arg Val Lys Thr Thr Ile Val Tyr Gly Arg Arg Arg  
260 265 270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser  
275 280 285

Pro Leu Pro Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg  
290 295 300

Glu  
305

<210> 139  
<211> 212  
<212> PRT  
<213> Haemophilus influenzae

<400> 139  
Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly  
1 5 10 15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe  
20 25 30

Phe Gly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asp Ser Glu  
35 40 45

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln  
50 55 60

Gly Tyr Thr Ala Met Gln Thr Pro Phe Thr Ile Thr Leu Glu Asn Cys  
65 70 75 80

Asn Val Thr Thr Thr Asn Asn Lys Pro Lys Ala Thr Lys Val Gly Val  
85 90 95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu  
100 105 110

Lys Asn Ile Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val  
115 120 125

Asn Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val  
130 135 140

Gly Lys Thr Thr Thr Asp Phe Thr Ser Glu Asn His Asn Gly Ala Gly  
145 150 155 160

Ala Asp Pro Val Ala Thr Asn Lys His Ile Ser Ser Leu Thr Pro Leu  
165 170 175

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Asn Asn Gln Asn Ser Ile Asn Leu His Tyr Ile Ala Gln Tyr Tyr Ala  
 180 185 190  
 Thr Gly Val Ala Glu Ala Gly Lys Val Pro Ser Ser Val Asn Ser Gln  
 195 200 205  
 Ile Ala Tyr Glu  
 210

<210> 140  
 <211> 139  
 <212> PRT  
 <213> Pseudomonas stutzeri

<400> 140  
 Met Lys Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile  
 1 5 10 15  
 Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr  
 20 25 30  
 Gln Asp Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile  
 35 40 45  
 Thr Pro Gly Lys Ile Gly Phe Glu Gln Ala Ile Asn Glu Gly Lys Thr  
 50 55 60  
 Pro Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser  
 65 70 75 80  
 Thr Ser Tyr Cys Asp Val Asp Leu Asp Thr Ala Ala Asp Gly His Ile  
 85 90 95  
 Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr  
 100 105 110  
 Ile Thr Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr  
 115 120 125  
 Leu Asp Ala Lys Tyr Lys Pro Gly Lys Cys Ser  
 130 135

<210> 141  
 <211> 59  
 <212> PRT  
 <213> Caulobacter crescentus

<400> 141  
 Met Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr  
 1 5 10 15  
 Ala Ile Glu Tyr Gly Leu Ile Val Ala Leu Ile Ala Val Val Ile Val  
 20 25 30  
 Thr Ala Val Thr Thr Leu Gly Thr Asn Leu Arg Thr Ala Phe Thr Lys  
 35 40 45  
 Ala Gly Ala Ala Val Ser Thr Ala Ala Gly Thr  
 50 55

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<210> 142  
 <211> 173  
 <212> PRT  
 <213> Escherichia coli

<400> 142  
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln  
 1 5 10 15  
 Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys  
 20 25 30  
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu  
 35 40 45  
 Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu  
 50 55 60  
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn  
 65 70 75 80  
 Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val  
 85 90 95  
 Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala  
 100 105 110  
 Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu  
 115 120 125  
 Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr  
 130 135 140  
 Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly  
 145 150 155 160  
 Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln  
 165 170

<210> 143  
 <211> 173  
 <212> PRT  
 <213> Escherichia coli

<400> 143  
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln  
 1 5 10 15  
 Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys  
 20 25 30  
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu  
 35 40 45  
 Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu  
 50 55 60  
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn  
 65 70 75 80  
 Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val  
 85 90 95

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Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala  
 100 105 110  
 Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu  
 115 120 125  
 Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr  
 130 135 140  
 Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly  
 145 150 155 160  
 Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln  
 165 170

<210> 144  
 <211> 172  
 <212> PRT  
 <213> Escherichia coli

<400> 144  
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln  
 1 5 10 15  
 Gly Gln Gly Arg Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys  
 20 25 30  
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu  
 35 40 45  
 Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu  
 50 55 60  
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn  
 65 70 75 80  
 Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser  
 85 90 95  
 Gly His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile  
 100 105 110  
 Met Ile Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly  
 115 120 125  
 Asp Pro Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr  
 130 135 140  
 Val Gly Lys Lys Ser Ser Asp Gly Asn Ala Gln Ile Thr Glu Gly Ala  
 145 150 155 160  
 Phe Ser Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln  
 165 170

<210> 145  
 <211> 853  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (281) .. (829)

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<400> 145
acgtttctgt ggctcgacgc atcttctctca ttcttctctc caaaaaccac ctcatgcaat 60
ataaacatct ataaataaag ataacaaata gaatattaag ccaacaaata aactgaaaaa 120
gtttgtccgc gatgctttac ctctatgagt caaaatggcc ccaatgtttc atcttttggg 180
ggaaactgtg cagtgttggc agtcaaactc gttgacaaac aaagtgtaca gaacgactgc 240
ccatgtcgat ttagaaatag ttttttgaaa ggaaagcagc atg aaa att aaa act 295
Met Lys Ile Lys Thr
1 5
ctg gca atc gtt gtt ctg tgc gct ctg tcc ctc agt tct acg acg gct 343
Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Ser Thr Thr Ala
10 15 20
ctg gcc gct gcc acg acg gtt aat ggt ggg acc gtt cac ttt aaa ggg 391
Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr Val His Phe Lys Gly
25 30 35
gaa gtt gtt aac gcc gct tgc gca gtt gat gca ggc tct gtt gat caa 439
Glu Val Val Val Asn Ala Ala Cys Ala Val Asp Ala Gly Ser Val Asp Gln
40 45 50
acc gtt cag tta gga cag gtt cgt acc gca tgc ctg gca cag gaa gga 487
Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly
55 60 65
gca acc agt tct gct gtc ggt ttt aac att cag ctg aat gat tgc gat 535
Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln Leu Asn Asp Cys Asp
70 75 80 85
acc aat gtt gca tct aaa gcc gct gtt gcc ttt tta ggt acg gcg att 583
Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe Leu Gly Thr Ala Ile
90 95 100
gat gcg ggt cat acc aac gtt ctg gct ctg cag agt tca gct gcg ggt 631
Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln Ser Ser Ala Ala Gly
105 110 115
agc gca aca aac gtt ggt gtg cag atc ctg gac aga acg ggt gct gcg 679
Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp Arg Thr Gly Ala Ala
120 125 130
ctg acg ctg gat ggt gcg aca ttt agt tca gaa aca acc ctg aat aac 727
Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu Thr Thr Leu Asn Asn
135 140 145
gga acc aat acc att ccg ttc cag gcg cgt tat ttt gca acc ggg gcc 775
Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala
150 155 160 165
gca acc ccg ggt gct gct aat gcg gat gcg acc ttc aag gtt cag tat 823
Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Gln Tyr
170 175 180
caa taa cctacctagg ttcagggacg ttca 853
Gln

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<210> 146

<211> 182

<212> PRT

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<213> Escherichia coli

<400> 146

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Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
 1          5          10          15
Ser Ser Thr Thr Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
          20          25          30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
          35          40          45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
          50          55          60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
          65          70          75          80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
          85          90          95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
          100          105          110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
          115          120          125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
          130          135          140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
          145          150          155          160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
          165          170          175
Phe Lys Val Gln Tyr Gln
          180

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<210> 147

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG peptide

<400> 147

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Cys Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
 1          5          10

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<210> 148

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 148

ccggaattca tggacattga cccttataaa g

31

<210> 149

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<400> 149  
gtgcagtatg gtgaggtgag gaatgctcag gagactc 37

<210> 150  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 150  
gsgtctcctg agcattcctc acctcaccat actgcac 37

<210> 151  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 151  
cttccaaaag tgagggaaga aatgtgaaac cac 33

<210> 152  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 152  
cgcgccccaa gcttctaaac aacagtagtc tccggaagcg ttgatag 47

<210> 153  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 153  
gtgggtttcac atttcttccc tcacttttgg aag 33

<210> 154  
<211> 281  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 154  
Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe  
1 5 10 15

Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser  
20 25 30

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Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe  
 35 40 45  
 Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn  
 50 55 60  
 Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala  
 65 70 75 80  
 Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser  
 85 90 95  
 Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn  
 100 105 110  
 Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile  
 115 120 125  
 Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser  
 130 135 140  
 Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr  
 145 150 155 160  
 Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr  
 165 170 175  
 Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val  
 180 185 190  
 Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr  
 195 200 205  
 Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ser  
 210 215 220  
 Ser Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg  
 225 230 235 240  
 Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys  
 245 250 255  
 Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala  
 260 265 270  
 Arg Leu Lys Lys Leu Val Gly Glu Arg  
 275 280  
 <210> 155  
 <211> 181  
 <212> PRT  
 <213> Escherichia coli  
 <400> 155  
 Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu  
 1 5 10 15  
 Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr  
 20 25 30  
 Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala  
 35 40 45.

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Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser  
50 55 60

Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln  
65 70 75 80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe  
85 90 95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln  
100 105 110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp  
115 120 125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu  
130 135 140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr  
145 150 155 160

Phe Ala Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe  
165 170 175

Lys Val Gln Tyr Gln  
180

<210> 156  
<211> 447  
<212> DNA  
<213> Hepatitis B

<220>  
<221> CDS  
<222> (1)..(447)

<400> 156  
atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc 48  
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

tgc ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctt cta gat 96  
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

acc gcc gca gct ctg tat cgg gat gcc tta gag tct cct gag cat tgt 144  
Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg gga gac 192  
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp  
50 55 60

tta atg act cta gct acc tgg gtg ggt act aat tta gaa gat cca gca 240  
Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala  
65 70 75 80

tct agg gac cta gta gtc agt tat gtc aac act aat gtg ggc cta aag 288  
Ser Arg Asp Leu Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys  
85 90 95

ttc aga caa tta ttg tgg ttt cac att tct tgt ctc act ttt gga aga 336  
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

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100	105	110	
gaa acg gtt cta gag tat ttg gtc tct ttt gga gtg tgg att cgc act			384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr			
115	120	125	
cct cca gcc tat aga cca cca aat gcc cct atc cta tca acg ctt ccg			432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro			
130	135	140	
gag act act gtt gtt			447
Glu Thr Thr Val Val			
145			

<210> 157  
 <211> 149  
 <212> PRT  
 <213> Hepatitis B

<400> 157  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala  
 65 70 75 80  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys  
 85 90 95  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Thr Val Val  
 145

<210> 158  
 <211> 152  
 <212> PRT  
 <213> Hepatitis B

<400> 158  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

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	20		25		30										
Thr	Ala	Ala	Ala	Leu	Tyr	Arg	Asp	Ala	Leu	Glu	Ser	Pro	Glu	His	Cys
	35						40					45			
Ser	Pro	His	His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu	Cys	Trp	Gly	Asp
	50					55					60				
Leu	Met	Thr	Leu	Ala	Thr	Trp	Val	Gly	Thr	Asn	Leu	Glu	Asp	Gly	Gly
65					70					75					80
Lys	Gly	Gly	Ser	Arg	Asp	Leu	Val	Val	Ser	Tyr	Val	Asn	Thr	Asn	Val
				85					90					95	
Gly	Leu	Lys	Phe	Arg	Gln	Leu	Leu	Trp	Phe	His	Ile	Ser	Cys	Leu	Thr
			100					105					110		
Phe	Gly	Arg	Glu	Thr	Val	Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp
		115					120					125			
Ile	Arg	Thr	Pro	Pro	Ala	Tyr	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser
	130					135					140				
Thr	Leu	Pro	Glu	Thr	Thr	Val	Val								
145					150										

<210> 159  
 <211> 132  
 <212> PRT  
 <213> Bacteriophage Q Beta

<400>	159														
Ala	Lys	Leu	Glu	Thr	Val	Thr	Leu	Gly	Asn	Ile	Gly	Lys	Asp	Gly	Lys
1				5					10					15	
Gln	Thr	Leu	Val	Leu	Asn	Pro	Arg	Gly	Val	Asn	Pro	Thr	Asn	Gly	Val
			20					25					30		
Ala	Ser	Leu	Ser	Gln	Ala	Gly	Ala	Val	Pro	Ala	Leu	Glu	Lys	Arg	Val
		35				40						45			
Thr	Val	Ser	Val	Ser	Gln	Pro	Ser	Arg	Asn	Arg	Lys	Asn	Tyr	Lys	Val
	50					55					60				
Gln	Val	Lys	Ile	Gln	Asn	Pro	Thr	Ala	Cys	Thr	Ala	Asn	Gly	Ser	Cys
65					70					75					80
Asp	Pro	Ser	Val	Thr	Arg	Gln	Ala	Tyr	Ala	Asp	Val	Thr	Phe	Ser	Phe
				85					90					95	
Thr	Gln	Tyr	Ser	Thr	Asp	Glu	Glu	Arg	Ala	Phe	Val	Arg	Thr	Glu	Leu
			100					105					110		
Ala	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Leu	Ile	Asp	Ala	Ile	Asp	Gln	Leu
		115					120					125			
Asn	Pro	Ala	Tyr												
	130														

<210> 160  
 <211> 129  
 <212> PRT

203.F0.20505001

<213> Bacteriophage R 17

<400> 160

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly  
1 5 10 15  
Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp  
20 25 30  
Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val  
35 40 45  
Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val  
50 55 60  
Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala  
65 70 75 80  
Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala  
85 90 95  
Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu  
100 105 110  
Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile  
115 120 125

Tyr

<210> 161

<211> 130

<212> PRT

<213> Bacteriophage fr

<400> 161

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr  
1 5 10 15  
Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
20 25 30  
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
35 40 45  
Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu  
50 55 60  
Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val  
65 70 75 80  
Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe  
85 90 95  
Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr  
100 105 110  
Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly  
115 120 125

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Ile Tyr  
130

<210> 162  
<211> 130  
<212> PRT  
<213> Bacteriophage GA

<400> 162

Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly  
1 5 10 15  
Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp  
20 25 30  
Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr  
35 40 45  
Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val  
50 55 60  
Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser  
65 70 75 80  
Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala  
85 90 95  
Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe  
100 105 110  
Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe  
115 120 125  
Tyr Ala  
130

<210> 163  
<211> 132  
<212> PRT  
<213> Bacteriophage SP

<400> 163

Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly  
1 5 10 15  
Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly  
20 25 30  
Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg  
35 40 45  
Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys  
50 55 60  
Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys  
65 70 75 80

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Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe  
85 90 95

Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu  
100 105 110

Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu  
115 120 125

Asn Pro Ala Tyr  
130

<210> 164  
<211> 130  
<212> PRT  
<213> Bacteriophage MS2

<400> 164

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr  
1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
115 120 125

Ile Tyr  
130

<210> 165  
<211> 133  
<212> PRT  
<213> Bacteriophage M11

<400> 165

Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly  
1 5 10 15

Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly  
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg  
35 40 45

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Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys  
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr  
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser  
85 90 95

Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu  
100 105 110

Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn  
115 120 125

Leu Asn Pro Ala Tyr  
130

<210> 166  
<211> 133  
<212> PRT  
<213> Bacteriophage MX1

<400> 166  
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly  
1 5 10 15

Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly  
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg  
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys  
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr  
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser  
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu  
100 105 110

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn  
115 120 125

Leu Asn Pro Ala Tyr  
130

<210> 167  
<211> 330  
<212> PRT  
<213> Bacteriophage NL95

<400> 167  
Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly  
1 5 10 15

Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly

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20					25					30					
Val	Ala	Ser	Leu	Ser	Glu	Ala	Gly	Ala	Val	Pro	Ala	Leu	Glu	Lys	Arg
		35					40					45			
Val	Thr	Val	Ser	Val	Ala	Gln	Pro	Ser	Arg	Asn	Arg	Lys	Asn	Tyr	Lys
	50					55					60				
Val	Gln	Ile	Lys	Leu	Gln	Asn	Pro	Thr	Ala	Cys	Thr	Lys	Asp	Ala	Cys
	65				70					75					80
Asp	Pro	Ser	Val	Thr	Arg	Ser	Gly	Ser	Arg	Asp	Val	Thr	Leu	Ser	Phe
				85					90					95	
Thr	Ser	Tyr	Ser	Thr	Glu	Arg	Glu	Arg	Ala	Leu	Ile	Arg	Thr	Glu	Leu
			100					105					110		
Ala	Ala	Leu	Leu	Lys	Asp	Asp	Leu	Ile	Val	Asp	Ala	Ile	Asp	Asn	Leu
		115					120					125			
Asn	Pro	Ala	Tyr	Trp	Ala	Ala	Leu	Leu	Ala	Ala	Ser	Pro	Gly	Gly	Gly
	130					135					140				
Asn	Asn	Pro	Tyr	Pro	Gly	Val	Pro	Asp	Ser	Pro	Asn	Val	Lys	Pro	Pro
	145				150					155					160
Gly	Gly	Thr	Gly	Thr	Tyr	Arg	Cys	Pro	Phe	Ala	Cys	Tyr	Arg	Arg	Gly
				165					170					175	
Glu	Leu	Ile	Thr	Glu	Ala	Lys	Asp	Gly	Ala	Cys	Ala	Leu	Tyr	Ala	Cys
			180					185					190		
Gly	Ser	Glu	Ala	Leu	Val	Glu	Phe	Glu	Tyr	Ala	Leu	Glu	Asp	Phe	Leu
		195					200					205			
Gly	Asn	Glu	Phe	Trp	Arg	Asn	Trp	Asp	Gly	Arg	Leu	Ser	Lys	Tyr	Asp
	210					215					220				
Ile	Glu	Thr	His	Arg	Arg	Cys	Arg	Gly	Asn	Gly	Tyr	Val	Asp	Leu	Asp
	225				230					235					240
Ala	Ser	Val	Met	Gln	Ser	Asp	Glu	Tyr	Val	Leu	Ser	Gly	Ala	Tyr	Asp
				245					250					255	
Val	Val	Lys	Met	Gln	Pro	Pro	Gly	Thr	Phe	Asp	Ser	Pro	Arg	Tyr	Tyr
			260					265					270		
Leu	His	Leu	Met	Asp	Gly	Ile	Tyr	Val	Asp	Leu	Ala	Glu	Val	Thr	Ala
		275					280					285			
Tyr	Arg	Ser	Tyr	Gly	Met	Val	Ile	Gly	Phe	Trp	Thr	Asp	Ser	Lys	Ser
	290					295					300				
Pro	Gln	Leu	Pro	Thr	Asp	Phe	Thr	Arg	Phe	Asn	Arg	His	Asn	Cys	Pro
	305				310					315					320
Val	Gln	Thr	Val	Ile	Val	Ile	Pro	Ser	Leu						
				325					330						

<210> 168  
 <211> 134  
 <212> PRT

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<213> Apis mellifera

<400> 168

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser  
1 5 10 15  
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg  
20 25 30  
Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His  
35 40 45  
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp  
50 55 60  
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser  
65 70 75 80  
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr  
85 90 95  
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg  
100 105 110  
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp  
115 120 125  
Phe Asp Leu Arg Lys Tyr  
130

<210> 169

<211> 129

<212> PRT

<213> Apis mellifera

<400> 169

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser  
1 5 10 15  
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg  
20 25 30  
Thr His Asp Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His  
35 40 45  
Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asn Asp Leu  
50 55 60  
Phe Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys  
65 70 75 80  
Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro  
85 90 95  
Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr  
100 105 110  
Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp Phe Asp Leu Arg Lys  
115 120 125  
Tyr

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<210> 170  
 <211> 134  
 <212> PRT  
 <213> Apis dorsata

<400> 170  
 Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser  
 1 5 10 15  
 Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg  
 20 25 30  
 Ser His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His  
 35 40 45  
 Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp  
 50 55 60  
 Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser  
 65 70 75 80  
 Tyr Phe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr  
 85 90 95  
 Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg  
 100 105 110  
 Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp  
 115 120 125  
 Phe Asp Leu Arg Lys Tyr  
 130

<210> 171  
 <211> 134  
 <212> PRT  
 <213> Apis cerana

<400> 171  
 Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser  
 1 5 10 15  
 Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg  
 20 25 30  
 Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His  
 35 40 45  
 Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp  
 50 55 60  
 Asp Thr Phe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser  
 65 70 75 80  
 Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr  
 85 90 95  
 Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg  
 100 105 110  
 Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp  
 115 120 125

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Phe Asp Leu Arg Lys Tyr  
130

<210> 172  
<211> 136  
<212> PRT  
<213> Bombus pennsylvanicus

<400> 172

Ile	Ile	Tyr	Pro	Gly	Thr	Leu	Trp	Cys	Gly	Asn	Gly	Asn	Ile	Ala	Asn	
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Gly	Thr	Asn	Glu	Leu	Gly	Leu	Trp	Lys	Glu	Thr	Asp	Ala	Cys	Cys	Arg	
		20						25					30			
Thr	His	Asp	Met	Cys	Pro	Asp	Ile	Ile	Glu	Ala	His	Gly	Ser	Lys	His	
		35					40					45				
Gly	Leu	Thr	Asn	Pro	Ala	Asp	Tyr	Thr	Arg	Leu	Asn	Cys	Glu	Cys	Asp	
	50					55					60					
Glu	Glu	Phe	Arg	His	Cys	Leu	His	Asn	Ser	Gly	Asp	Ala	Val	Ser	Ala	
65				70						75					80	
Ala	Phe	Val	Gly	Arg	Thr	Tyr	Phe	Thr	Ile	Leu	Gly	Thr	Gln	Cys	Phe	
				85					90					95		
Arg	Leu	Asp	Tyr	Pro	Ile	Val	Lys	Cys	Lys	Val	Lys	Ser	Thr	Ile	Leu	
			100					105					110			
Arg	Glu	Cys	Lys	Glu	Tyr	Glu	Phe	Asp	Thr	Asn	Ala	Pro	Gln	Lys	Tyr	
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Gln	Trp	Phe	Asp	Val	Leu	Ser	Tyr									
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<210> 173  
<211> 142  
<212> PRT  
<213> Heloderma suspectum

<400> 173

Gly	Ala	Phe	Ile	Met	Pro	Gly	Thr	Leu	Trp	Cys	Gly	Ala	Gly	Asn	Ala	
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Ala	Ser	Asp	Tyr	Ser	Gln	Leu	Gly	Thr	Glu	Lys	Asp	Thr	Asp	Met	Cys	
		20						25					30			
Cys	Arg	Asp	His	Asp	His	Cys	Ser	Asp	Thr	Met	Ala	Ala	Leu	Glu	Tyr	
		35					40					45				
Lys	His	Gly	Met	Arg	Asn	Tyr	Arg	Pro	His	Thr	Val	Ser	His	Cys	Asp	
	50					55					60					
Cys	Asp	Asn	Gln	Phe	Arg	Ser	Cys	Leu	Met	Asn	Val	Lys	Asp	Arg	Thr	
65				70						75				80		
Ala	Asp	Leu	Val	Gly	Met	Thr	Tyr	Phe	Thr	Val	Leu	Lys	Ile	Ser	Cys	
				85					90					95		

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Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Asn Asn Phe Ser Gln  
 100 105 110  
 Gln Cys Thr Lys Ser Glu Ile Met Pro Val Ala Lys Leu Val Ser Ala  
 115 120 125  
 Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly  
 130 135 140

<210> 174  
 <211> 143  
 <212> PRT  
 <213> Heloderma suspectum

<400> 174  
 Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala  
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 Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys  
 20 25 30  
 Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr  
 35 40 45  
 Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp  
 50 55 60  
 Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr  
 65 70 75 80  
 Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys  
 85 90 95  
 Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Trp Asn Phe Trp Leu  
 100 105 110  
 Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala  
 115 120 125  
 Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly Arg  
 130 135 140

<210> 175  
 <211> 142  
 <212> PRT  
 <213> Heloderma suspectum

<400> 175  
 Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala  
 1 5 10 15  
 Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys  
 20 25 30  
 Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr  
 35 40 45  
 Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp  
 50 55 60  
 Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr

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65					70						75				80
Ala	Asp	Tyr	Val	Gly	Gln	Thr	Tyr	Phe	Asn	Val	Leu	Lys	Ile	Pro	Cys
				85					90					95	
Phe	Glu	Leu	Glu	Glu	Gly	Glu	Gly	Cys	Val	Asp	Trp	Asn	Phe	Trp	Leu
			100					105					110		
Glu	Cys	Thr	Glu	Ser	Lys	Ile	Met	Pro	Val	Ala	Lys	Leu	Val	Ser	Ala
		115					120					125			
Ala	Pro	Tyr	Gln	Ala	Gln	Ala	Glu	Thr	Gln	Ser	Gly	Glu	Gly		
	130					135					140				

<210> 176  
 <211> 574  
 <212> PRT  
 <213> IgE heavy chain

<400> 176

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His	Ser	Gln	Thr	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Arg	Lys	Pro
			20					25					30		
Gly	Ala	Ser	Val	Arg	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ile
		35					40					45			
Asp	Ser	Tyr	Ile	His	Trp	Ile	Arg	Gln	Ala	Pro	Gly	His	Gly	Leu	Glu
	50					55					60				
Trp	Val	Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Pro
65					70					75					80
Arg	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Ala	Ser	Phe	Ser	Thr
				85					90					95	
Ala	Tyr	Met	Asp	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Ser	Ala	Val	Phe
			100					105					110		
Tyr	Cys	Ala	Lys	Ser	Asp	Pro	Phe	Trp	Ser	Asp	Tyr	Tyr	Asn	Phe	Asp
		115					120					125			
Tyr	Ser	Tyr	Thr	Leu	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
	130					135					140				
Ser	Ser	Ala	Ser	Thr	Gln	Ser	Pro	Ser	Val	Phe	Pro	Leu	Thr	Arg	Cys
145					150					155					160
Cys	Lys	Asn	Ile	Pro	Ser	Asn	Ala	Thr	Ser	Val	Thr	Leu	Gly	Cys	Leu
				165					170				175		
Ala	Thr	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Met	Val	Thr	Trp	Asp	Thr	Gly
			180					185					190		
Ser	Leu	Asn	Gly	Thr	Thr	Met	Thr	Leu	Pro	Ala	Thr	Thr	Leu	Thr	Leu
		195					200					205			
Ser	Gly	His	Tyr	Ala	Thr	Ile	Ser	Leu	Leu	Thr	Val	Ser	Gly	Ala	Trp
	210					215					220				

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Ala	Lys	Gln	Met	Phe	Thr	Cys	Arg	Val	Ala	His	Thr	Pro	Ser	Ser	Thr
225					230					235					240
Asp	Trp	Val	Asp	Asn	Lys	Thr	Phe	Ser	Val	Cys	Ser	Arg	Asp	Phe	Thr
				245					250					255	
Pro	Pro	Thr	Val	Lys	Ile	Leu	Gln	Ser	Ser	Cys	Asp	Gly	Gly	Gly	His
			260					265					270		
Phe	Pro	Pro	Thr	Ile	Gln	Leu	Leu	Cys	Leu	Val	Ser	Gly	Tyr	Thr	Pro
		275					280					285			
Gly	Thr	Ile	Asn	Ile	Thr	Trp	Leu	Glu	Asp	Gly	Gln	Val	Met	Asp	Val
	290					295					300				
Asp	Leu	Ser	Thr	Ala	Ser	Thr	Thr	Gln	Glu	Gly	Glu	Leu	Ala	Ser	Thr
305					310					315					320
Gln	Ser	Glu	Leu	Thr	Leu	Ser	Gln	Lys	His	Trp	Leu	Ser	Asp	Arg	Thr
				325					330					335	
Tyr	Thr	Cys	Gln	Val	Thr	Tyr	Gln	Gly	His	Thr	Phe	Glu	Asp	Ser	Thr
			340					345					350		
Lys	Lys	Cys	Ala	Asp	Ser	Asn	Pro	Arg	Gly	Val	Ser	Ala	Tyr	Leu	Ser
		355					360					365			
Arg	Pro	Ser	Pro	Phe	Asp	Leu	Phe	Ile	Arg	Lys	Ser	Pro	Thr	Ile	Thr
	370					375					380				
Cys	Leu	Val	Val	Asp	Leu	Ala	Pro	Ser	Lys	Gly	Thr	Val	Asn	Leu	Thr
385					390					395				400	
Trp	Ser	Arg	Ala	Ser	Gly	Lys	Pro	Val	Asn	His	Ser	Thr	Arg	Lys	Glu
				405					410					415	
Glu	Lys	Gln	Arg	Asn	Gly	Thr	Leu	Thr	Val	Thr	Ser	Thr	Leu	Pro	Val
			420					425					430		
Gly	Thr	Arg	Asp	Trp	Ile	Glu	Gly	Glu	Thr	Tyr	Gln	Cys	Arg	Val	Thr
		435					440					445			
His	Pro	His	Leu	Pro	Arg	Ala	Leu	Met	Arg	Ser	Thr	Thr	Lys	Thr	Ser
	450					455					460				
Gly	Pro	Arg	Ala	Ala	Pro	Glu	Val	Tyr	Ala	Phe	Ala	Thr	Pro	Glu	Trp
465					470					475					480
Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	Ala	Cys	Leu	Ile	Gln	Asn	Phe
				485					490					495	
Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	Trp	Leu	His	Asn	Glu	Val	Gln	Leu
			500					505					510		
Pro	Asp	Ala	Arg	His	Ser	Thr	Thr	Gln	Pro	Arg	Lys	Thr	Lys	Gly	Ser
		515					520					525			
Gly	Phe	Phe	Val	Phe	Ser	Arg	Leu	Glu	Val	Thr	Arg	Ala	Glu	Trp	Glu
	530					535					540				
Gln	Lys	Asp	Glu	Phe	Ile	Cys	Arg	Ala	Val	His	Glu	Ala	Ala	Ser	Pro
545					550					555					560

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Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys  
565 570

<210> 177

<400> 177  
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<210> 178  
<211> 13  
<212> PRT  
<213> IgE Peptides

<400> 178  
Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly  
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<210> 179  
<211> 8  
<212> PRT  
<213> IgE Mimotype

<400> 179  
Ile Asn His Arg Gly Tyr Trp Val  
1 5

<210> 180  
<211> 8  
<212> PRT  
<213> IgE Mimotype

<400> 180  
Arg Asn His Arg Gly Tyr Trp Val  
1 5

<210> 181  
<211> 10  
<212> PRT  
<213> IgE Mimotype

<400> 181

Arg Ser Arg Ser Gly Gly Tyr Trp Leu Trp  
1 5 10

<210> 182  
<211> 10  
<212> PRT  
<213> IgE Mimotype

<400> 182  
Val Asn Leu Thr Trp Ser Arg Ala Ser Gly  
1 5 10

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<210> 183  
 <211> 10  
 <212> PRT  
 <213> IgE Mimotype

<400> 183  
 Val Asn Leu Pro Trp Ser Arg Ala Ser Gly  
 1 5 10

<210> 184  
 <211> 10  
 <212> PRT  
 <213> IgE Mimotype

<400> 184  
 Val Asn Leu Thr Trp Ser Phe Gly Leu Glu  
 1 5 10

<210> 185  
 <211> 10  
 <212> PRT  
 <213> IgE Mimotype

<400> 185  
 Val Asn Leu Pro Trp Ser Phe Gly Leu Glu  
 1 5 10

<210> 186  
 <211> 10  
 <212> PRT  
 <213> IgE Mimotype

<400> 186  
 Val Asn Arg Pro Trp Ser Phe Gly Leu Glu  
 1 5 10

<210> 187  
 <211> 10  
 <212> PRT  
 <213> IgE Mimotype

<400> 187  
 Val Lys Leu Pro Trp Arg Phe Tyr Gln Val  
 1 5 10

<210> 188  
 <211> 10  
 <212> PRT  
 <213> IgE Mimotype

<400> 188  
 Val Trp Thr Ala Cys Gly Tyr Gly Arg Met  
 1 5 10

<210> 189  
 <211> 7

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<212> PRT  
<213> IgE Mimotype

<400> 189  
Gly Thr Val Ser Thr Leu Ser  
1 5

<210> 190  
<211> 7  
<212> PRT  
<213> IgE Mimotype

<400> 190  
Leu Leu Asp Ser Arg Tyr Trp  
1 5

<210> 191  
<211> 7  
<212> PRT  
<213> IgE Mimotype

<400> 191  
Gln Pro Ala His Ser Leu Gly  
1 5

<210> 192  
<211> 7  
<212> PRT  
<213> IgE Mimotype

<400> 192  
Leu Trp Gly Met Gln Gly Arg  
1 5

<210> 193  
<211> 15  
<212> PRT  
<213> IgE Mimotype

<400> 193  
Leu Thr Leu Ser His Pro His Trp Val Leu Asn His Phe Val Ser  
1 5 10 15

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Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His  
 275 280 285  
 Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly  
 290 295 300  
 Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile  
 305 310 315 320  
 Gln Ala Val Ile Val Val Pro Arg Ala  
 325

<210> 218

<211> 770

<212> PRT

<213> Amyloid-Beta Protein (Homo Sapiens)

<400> 218

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
 1 5 10 15  
 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
 20 25 30  
 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80  
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125  
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
 130 135 140  
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
 145 150 155 160  
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
 165 170 175  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
 180 185 190  
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
 195 200 205

10050502 011302

Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
210						215					220				
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
				245					250					255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
			260					265					270		
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
		275					280					285			
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
290						295					300				
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
305					310					315					320
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
				325					330					335	
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr
			340					345					350		
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala
		355					360					365			
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp
		370				375					380				
Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala
385					390					395					400
Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala
				405					410					415	
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile
			420					425					430		
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn
		435					440					445			
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met
		450				455					460				
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu
465					470					475					480
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys
				485					490					495	
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe
			500					505					510		
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser
		515					520					525			
Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser
		530				535					540				

1005002 011802

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn  
770

<210> 219

<211> 82

<212> PRT

<213> Beta-Amyloid Peptide Precursor (Homo Sapiens)

<400> 219

Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys  
1 5 10 15

Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln  
20 25 30

"20250507" 20250507

Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile  
35 40 45  
Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile  
50 55 60  
Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val  
65 70 75 80  
Val Glu

<210> 220

<211> 42

<212> PRT

<213> Amyloid Beta Peptide

<400> 220

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
1 5 10 15  
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile  
20 25 30  
Gly Leu Met Val Gly Gly Val Val Ile Ala  
35 40

221:

RANKL\_human: TrEMBL:O14788: extracellular domain

YFRAQMDPNRIS EDGTHCIYRI LRLHENADFQ DTTLESQDTK LIPDSCRRIK QAFQGA VQKE  
LQHIVGSQHI RAEKAMVDGS WDLAKRSKL EAQPF AHLTINATDIPSGSH KVSLSWYHD  
RGWAKISNMT FSNGKLIVNQ DGFYYLYANI CFRHHETSGD LATEYLQLMV YVTKTSIKIP  
SSHTLMKGG S TKYWSGNSEF HFYSINVGGF FKLRSGEEIS IEVSNPSLLD PDQDATYFGA FKVRDID

222:

RANKL\_human: spliced isoformTrEMBL:O14788

MDPNRI SEDG THCIYRILRL HENADFQDTT LESQDTKLIP DSCRRIKQAF QGAVQKELQH  
IVGSQHIRAE KAMVDGSWLD LAKRSKLEAQ PFAHLTINAT DIPSGSHKVS LSSWYH DRGW  
AKISNMTFSN GKLIVNQDGF YYLYANICFR HHETSGDLAT EYLQLMVYVT KTSIKIPSSH  
TLMKGGSTKY WSGNSEFHFY SINVG GFFKL RSGEEISIEV SNPSLLDPDQ DATYFGAFKV  
RDID

223:

RANKL\_mouse: TrEMBL:O35235: extracellular domain

YFRAQMDPNRI SEDSTHCFYR ILRLHENAGL QDSTLESED TLPDSCR RMKQ AFQGA VQKEL  
QHIVGPQRFS GAPAMMEGSW LDVAQRGKPE AQPF AHLTIN AASIPSGSHK VTLSSWYHDR

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GWAKISNMTL SNGKLRVNQD GFYYLYANIC FRHHETSGSV PTDYLQLMVY VVKTSIKIPS  
SHNLMKGGST KNWSGNSEFH FYSINVG GFF KLRAGEEISI QVSNPSLLDP DQDATYFGAF KVQDID

224:

**RANKL\_mouse spliced isoforms: TrEMBL:Q9JJK8**

MKQAFQGA VQ KELQHIVGPQ RFSGAPAMME GSWLDVAQRG KPEAQPF AHL TINAASIPSG  
SHKVTLS SWY HDRGWAKISN MTL SNGKLRV NQDGFYYLYA NICFRHHETS GSVPTDYLQL  
MVYVVKTSIK IPSSHNL MKG GSTKNWSGNS EFHFYSINVG GFFKLRAGEE ISIQVSNPSL  
LDPDQDATYF GAFKVQDID

225:

**MIF\_rat: SwissProt**

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTSDPCALCS  
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYYD MNAANVGWNG STFA

226:

**MIF\_mouse: SwissProt**

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTNDPCALCS  
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYYD MNAANVGWNG STFA

227:

**MIF\_human: SwissProt**

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFA

228:

**Human IL-17**

ACCESSION #: AAC50341

1 mtpgktslvs lllllsleai vkagitiprn pgcpnsedkn fprtvmvnln i hnrntntnp  
61 krssdyynrs tspwnlhrne dperypsviw eakcrhl gci nadgnvdyhm nsvpiqqeil  
121 vlrrepphpc nsfrlekilv svgctcvtpi vhhva

229:

**Mouse IL-17**

ACCESSION #: AAA37490

1 mspgrassvs lmlllllsla atvkaaa iip qssacpntea kdflqnvkvn lkvfnslgak  
61 vssrpsdyl nrstspwtlh rnedpdryps viweaqcrhq rcvnaegkld hhmnsqliqq  
121 eilvlkrepe scpftfrvek mlvgvgctcv asivrqa a

230:

**Human IL-13 (precursor)**

20050902 0130

MALLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSG  
CSAIEKTQRMMSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFN

231:

Human IL-13 (processed)

GPVPPSTALR ELIEELVNIT QNQKAPLCNG SMVWSINLTA  
GMYCAALES INVSAGSAIE KTQRMMSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL  
HLKKLFREGR FN

232:

Mouse IL-13 (processed)

GPVPRSVSLPLTLKELIEELSNIQDQTPLCNGSMVWSVDLAAGGFCVALDSLNTNISNCNAIYRTQRILHGLCNR  
KAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

233:

Human IL-5 (precursor)

MRMLLHLSLL ALGAAYVYAI PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH  
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQEFGLGVMNTEW  
IIES

234:

Human IL-5 (processed)

I PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH  
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQ  
EFLGVMNTEW IIES

235:

Mouse IL-5 (processed)

MEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRGGTVEMLFQNLSLIKK  
YIDRQKEKCGEERRRTRQFLDYLQEFGLGVMSTEWAMEG

236:

CCL21 Swissprot: SY21\_human: Sequence after cleavage of signal peptide:

SDGGAQD CLKYSQRKI PAKVVRSYRK QEPSLGCSIP AILFLPRKRS QAELCADPKE LWVQQLMQHL  
DKTPSPQKPA QGCRKDRGAS KTGKKGKGSK GCKRTERSQT PKGP

237:

CCL21 Swissprot: SY21\_mouse: Sequence after cleavage of signal peptide:

SDGGGQD CLKYSQKKI PYSIVRGYRK QEPSLGCPIP AILFSRPHS KPCLCANPEE GWVQNLMRRL

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DQPPAPGKQS PGCRCNRGTS KSGKKGKGSK GCKRTEQTQP SRG

238:

Swissprot: SDF1\_human: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHVA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ  
EYLEKALNKR FKM

239:

Swissprot: SDF1\_mouse: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHIA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ  
EYLEKALNK

240:

BLC Sequences: Human: Accession: NP\_006410

Amino acids 1-22 are signal peptide.

MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNGC  
PRKEIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

241:

BLC Sequence Mouse: accession: NP\_061354

Amino acids 1-21 are signal peptide

MRLSTATLLL LLASCLSPGH GILEAHYTNL KCRCSGVIST VVGLNIIDRI QVTPPGNGCP  
KTEVVIWTKM KKVICVNPR KWLQRLLRHV QSKSLSSTPQ APVSKRRAA

242:

Human Eotaxin-1

1-23 is Signal peptide

1 mkvsaallwl lliaaafspq glagpasvpt tccfnlanrk iplqrlesyr ritsgkcpqk  
61 avifkttklak dicadpkkkw vqdsmyldq ksptpkp

243:

Human Eotaxin-2

1-26 is Signal peptide

1 maglmtivts llflgvcahh iiptgsvvip spccmffvsk ripenrvvsv qlssrstclk  
61 agvifttkkkg qqfcgdpkqe wvqymknld akqkkaspra ravavkgpvq rypgnqtte

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244:

Human Eotaxin-3

1-23 is signal peptide

1 mmglslasav llasllslhl gtatrgsdis ktccfqyshk plpwtwvrsy eftsnscsqr  
61 avifttkrgk kvcthprkkw vqkyisllkt pkql

245:

Mouse Eotaxin-1

1-23 is signal peptide

1 mqsstallfl lltvtsftsq vlahpgsipt sccfimtskk ipntllksyk ritnnrctlk  
61 aivfktrlgk eicadpkkkw vqdatkhldq klqtpkp

246:

Mouse Eotaxin-2

1-25 is signal peptide

1 magsativag llllvacacc ifpidsvtip sscctsfisk kipenrvvsv qlangsicpk  
61 agvifitkkg hkictdpkll wvqrhiqkld akknqpskga kavrtkfavq rrrgnstev

247:

M-CSF Sequence: human: the construct would be an N-terminal fragment consisting of residue 33 -181 or 33 -185, corresponding to the soluble form of the receptor.

Accession: NP\_000748

MTAPGAAGRC	PPTTWLGSLL	LLVCLLASRS	ITEEVSEYCS	HMIGSGHLQS	LQRLIDSQME
TSCQITFEFV	DQEQLKDPVC	YLKKAFLLVQ	DIMEDTMRFR	DNTPNAIAIV	QLQELSLRLK
SCFTKDYEEL	DKACVRTFYE	TPLQLLEKVK	NVFNETKNLL	DKDWNIFSKN	CNNSFAECSS
QDVVTKPDCN	CLYPKAIPSS	DPASVSPHQP	LAPSMAPVAG	LTWEDSEGTE	GSSLLPGEQP
LHTVDPGSAK	QRPPRSTCQS	FEPPETPVVK	DSTIGGSPQP	RPSVGAFNPG	MEDILDSAMG
TNWVPEEASG	EASEIPVPQG	TELSPSRPGG	GSMQTEPARP	SNFLSASSPL	PASAKGQOPA
DVTGTALPRV	GPVRPTGQDW	NHTPQKTDHP	SALLRDPPEP	GSPIRSSPRP	QGLSNPSTLS
AQPQLSRSHS	SGSVLPLGEL	EGRRSTRDRR	SPAEPEGGPA	SEGAARPLPR	FNSVPLTDTH
ERQSEGSSSP	QLQESVFHLL	VPSVILVLLA	VGGLLFYRWR	RRSHQEPQRA	DSPLEQPEGS
PLTQDDRQVE	LPV				

248:

M-CSF Mouse sequence: Mature sequence starts at amino acid 33. Accession. NP\_031804

MTARGAAGRC	PSSTWLGSRL	LLVCLLMSRS	IAKEVSEHCS	HMIGNHGLKV	LQQLIDSQME
TSCQIAFEFV	DQEQLDDPVC	YLKKAFFLVQ	DIIDETMRFK	DNTPNANATE	RLQELSNNLN
SCFTKDYEEL	NKACVRTFHE	TPLQLLEKIK	NFFNETKNLL	EKDOWNIFTN	CNNSFAKCSS
RDVVTKPDCN	CLYPKATPSS	DPASASPHQP	PAPSMAPLAG	LAWDDSQRTE	GSSLLPSELP
LRIEDPGSAK	QRPPRSTCQT	LESTEQPNHG	DRLTEDSQPH	PSAGGPVPGV	EDILESSLGT
NWVLEEASGE	ASEGFLTQEA	KFSPSTPVGG	SIQAETDRPR	ALSASPFPKS	TEDQKPVDDIT

20250902 0:43:00

DRPLTEVNPM RPIGQTQNNNT PEKTDGTSTL REDHQEPGSP HIATPNPQRV SNSATPVAQL  
LLPKSHSWG I VLPLGELEGK RSTRDRRSPA ELEGGSASEG AARPVARFNS IPLTDTGHVE  
QHEGSSDPQI PESVFHLLVP GIILVLLTVG GLLFYKWKWR SHRDPQTLDS SVGRPEDSSL  
TQDEDRQVEL PV

249:

Sequence of Human Resistin: Precursor.

MKALCLLLLPLVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECSVTSRGDLATCPRGFAVTGCTCG  
SACGSWDVRAETTHCQCAGMDWTGARCCRVQP

250:

Sequence of Mouse Resistin: Precursor.

MKNLSFPLFLFLLVPELLGSSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSC  
GSACGSWDIREEKVCHCQCARIDWTAARCKLQVAS

251:

Lymphotoxin- $\beta$ :

Swissprot: TNFC\_human: Sequence of the extracellular domain:

QD QGGLVTETAD PGAQAQQGLG FQKLPEEEPE TDLSPGLPAA HLIGAPLKGQ GLGWETTKEQ  
AFLTSGTQFS DAEGALPQD GLYYLYCLVG YRGRAPPGGG DPQGRSVTLR SSLYRAGGAY GPGTPELLE  
GAETVTPVLD PARRQYGPL WYTSVGFGGL VQLRRGERVY VN

252:

Lymphotoxin- $\beta$ :

Swissprot: TNFC\_mouse: Sequence of the extracellular domain:

QD QGRRVEKIIG SGAQAQKRLD DSKPSCILPS PSSLSETPDP RLHPQRSNAS RNLASTSQGP  
VAQSSREASA WMTILSPAAD STPDGVQQL PKGEPETDLN PELPAAHLIG AWMSGQGLSW  
EASQEEAFRL SGAQFSPTHG LALPDGVVY LYCHVGYRGR TPPAGRSRAR SLTLRSALYR  
AGGAYGRGSP ELLLEGAETV TPVVDPIYG SLWYTSVGFG GLAQLRSGER VYVNISHPDM  
VDYRRGKTFF GAVMVG

253:

RNA-phage PP7:

mktivlsvg eatrtlteiq stadrqifee kvgplvgrlr ltaslrqnga ktayrvnlkl  
dqadvdcst svcgelpkvr ytvqvwshdvt ivansteasr kslydltksl vatsqvedlv  
vnlvplgr

254:

RNA-phage SP A1 protein:

2025-04-09 10:50:00

aklnqvtils kigkngdqt1 tltprgvnpt ngvaslseag avpalekrvt vsvaqpsrnr  
knfkvqiklq nptactrdac dpsvtrsafa dvtilsftsys tdeeralirt elaalladpl  
ivdaidnlnp aywaallvas sgggdnpsdp dvpvvpdvkp pdgtgrykcp facyrlgsiy  
evgkegspdi yergdevsvt fdyaledflg ntnwrnwdqr lsdydianrr rcrngnyidl  
datamqsddf vlsgrygvrk vkfpgafgsi kyllniqgda wldlsevtay rsygmvigfw  
tdskspqlpt dftqfnsanc pvqtviiips 1

255:

“Qβ 240”:

AKLETVTTLGNIG**RD**GKQTLVLNPRGVNPTNGVASLSQAGAVP  
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ  
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

256:

“Qβ 243”:

AKLETVTTLGKIGKD**G**KQTLVLNPRGVNPTNGVASLSQAGAVP  
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ  
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

257:

“Qβ 250”:

**AR**LETVTTLGNIG**RD**GKQTLVLNPRGVNPTNGVASLSQAGAVP  
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ  
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

258:

“Qβ 259”:

ARLETVTTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP  
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ  
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

259:

“Qβ 251”:

AKLETVTTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP  
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ  
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

260:

PH19 (SEQ ID NO:260)

20250902-041802

TAAGTCCTCTGCCACGTACC

261:

PH20 (SEQ ID NO:261)

TGGAAACCACGCTCACTTCC

262:

PH21 (SEQ ID NO:262)

CGGGATCCGGGATGAAGAACCTTTCATTTC

263:

PH22 (SEQ ID NO:263)

GCCTCTAGAGAGGAAGCGACCTGCAGCTTAC

264:

PH29 (SEQ ID NO:264)

CTAGCGGGAGGGGGTGGATGTGGGGACGACTACAAGGATGACGACA

265:

PH30 (SEQ ID NO:265)

AGCTTGTCGTCATCCTTG TAGTCGTCCCCACATCCACCCCCTCCCG

266:

PH31 (SEQ ID NO:266)

AGCTTACTCACACATGCCACCGTGCCCAGCACCTGAAGCCGAGG

267:

PH32 (SEQ ID NO:267)

CGGCTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTA

268:

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PH35 (SEQ ID NO:268)

CTAGCGGGAGGGGGTGGATGTGGGATCGAAGGTCGCA

269:

PH36 (SEQ ID NO:269)

AGCTTGCGACCTTCGATCCCACATCCACCCCCTCCCG

270:

PH37 (SEQ ID NO:270)

CGGGATCCAGCAGCTGGGCTCGAGGTGCTAGCTTTGTTTAAAC

271:

PH38 (SEQ ID NO:271)

GATCGTTTAAACAAACAAAGCTAGCACCTCGAGCCCAGCTGCTGGATCCCGGTAC

272:

PH39 (SEQ ID NO:272)

CTAGCGGGAGGGGGTGGATGTGGGGACGATGACGACA

273:

PH40 (SEQ ID NO:273)

AGCTTGTCGTCATCGTCCCCACATCCACCCCCTCCCG

274:

PH41 (SEQ ID NO:274)

CATGGAGACAGACACACTCCTGCTATGGGT

275:

PH42 (SEQ ID NO:275)

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GCAGTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTAC

276:

PH43 (SEQ ID NO:276)

ACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACGCG

277:

PH44 (SEQ ID NO:277)

GATCCGCGTCACCAGTGGAACCTGGAACCCAGAGCA

278:

SU7 (SEQ ID NO:278)

AGCTTGCGGATCCAGGATATCGGCTCGAGGTTCTAGAGTG

279:

SU8 (SEQ ID NO:279)

GGCCCACTCTAGAACCTCGAGCCGATATCCTGGATCCGCA

280:

Resistin-C-Xa:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG  
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCGIEGR

281:

Resistin-C-EK

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG  
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCGDDDD

282:

Resistin-GCG:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG  
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCG

2025-09-20 10:00:00

283:

pCep-Xa-Fc\*: (complete sequence)

```

1  GCCCCGCCGC CGGACGAACT AAACCTGACT ACGGCATCTC TGCCCCCTCT TCGCTGGTAC GAGGAGCGCT
71  TTTGTTTTGT ATTGGGGGCA GTGCATGTAA TCCCTTCAGT TGGTTGGTAC AACTTGCCAA CTGGGCGCTG
141  TTCCACATGT GACACGGGGG GGGACCAAAC ACAAGGGGT TCTCTGACTG TAGTTGACAT CCTTATAAAT
211  GGATGTGCAC ATTTGCCAAC ACTGAGTGGC TTTCATCTCT GAGCAGACTT TGCATGCTGT GGACTGCAAC
281  ACAACATTGC CTTTATGTGT AACTCTTGGC TGAAGCTCTT ACACCAATGC TGGGGGACAT GTACCTCCCA
351  GGGGCCACAG AAGACTACGG GAGGCTACAC CAACGTCAT CAGAGGGGCC TGTGTAGCTA CCGATAAGCG
421  GACCCTCAAG AGGGCATTAG CAATAGTGT TATAAGGCCC CCTGTTAAC CTAACGGG TAGCATATGC
491  TTCCCGGGTA GTAGTATATA CTATCCAGAC TAACCTAAT TCAATAGCAT ATGTTACCCA ACGGGAAGCA
561  TATGCTATCG AATTAGGGTT AGTAAAAGGG TCCTAAGGAA CAGCGATATC TCCCACCCA TGAGCTGTCA
631  CGGTTTTATT TACATGGGGT CAGGATTCCA CGAGGTTAGT GAACCATTTT AGTCACAAGG GCAGTGGCTG
701  AAGATCAAGG AGCGGGCAGT GAACCTCTCT GAATCTTCGC CTGCTCTCTC ATTCTCCTTC GTTTAGCTAA
771  TAGAATAACT GCTGAGTTGT GAACAGTAAG GTGTATGTGA GGTGCTCGAA AACAAAGGTTT CAGGTGACGC
841  CCCCAGAATA AAATTTGGAC GGGGGTTTCA TGTGTCCGAT TGTGCTATGA CACCAATATA ACCCTCACAA
911  ACCCTTGGG CAATAAATAC TAGTTAGGA ATGAAACATT CTGAATATCT TTAACAATAG AAATCCATGG
981  GGTGGGGACA AGCGTAAAG ACTGGATGTC CATCTCACAC GAATTTATGG CTATGGGCAA CACATAATCC
1051 TAGTGCAATA TGATACTGGG GTTATTAAGA TGTGTCCGAT TGTGCTATGA CACCAATATA ACCCTCACAA
1121 TACACTCTAT TTGTAACAAG GGGAAAGAGA TGGGACGCGG ACAGCAGCGG ACTCCACTGG TGTCTCTTAA
1191 CACCCCGGAA AATTAAACGG GGTCCACGCG CAATGGGGCC CATAAACAAA GACAAGTGGC CACTCTTTT
1261 TTTGAAATTT TGGAGTGGGG GCACGCGTCA GCCCCACAC GCGGTCAAAC CACTTGCCCA CAAAACCACT
1331 GGTGTGTAATA ACTTGGCTGA TTGTAACCCC TAGTATAGGA ATGAAACATT CTGAATATCT TTAACAATAG AAATCCATGG
1401 AATGGCACCC CGGGGAATAC CTGCATAAGT AGGTGGGCGG GCCAAGATAG GGGCGCGATT GCTGCGATCT
1471 GGAGGACAAA TTACACACAC TTGCGCCTGA GCGCCAAGCA CAGGTTGTTT GGTCTCTATA TTCACGAGGT
1541 CGCTGAGAGC ACGGTGGGCT AATGTTGCCA TGGGTAGCAT ATACTACCCA AATATCTGGA TAGCATATGC
1611 TATCTTAATC TATATCTGGG TAGCATAGGC TATCTTAATC TATATCTGGG TAGCATATGC TATCTTAATC
1681 TATATCTGGG TAGTATATGC TATCTTAATC TATATCTGGG TAGCATATGC TATCTTAATC TATATCTGGG
1751 TAGCATATGC TATCTTAATC TATATCTGGG TAGTATATGC TATCTTAATC TATATCTGGG TAGCATATGC
1821 TATCTTAATA GAGATTAGGG TAGTATATGC TATCTTAATC TATATCTGGG TAGCATATGC TATCTTAATC
1891 TCTGGATAGC ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC
1961 ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC
2031 CTAATTTATA TCTGGGTAGC ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA
2101 TCTGGGTAGT ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC
2171 ATATGATACC CAGTAGTAGA GTGGGAGTGC TATCTTTGTC ATATGCTATC CTAATCTATA TCTGGGTAGC
2241 TTTTCTGCTG TTGCTCTTTT CCTGCATGCT GTTCTGCTCC ATTTCTAGGT GAATTTAAGG AGGCCAGGCT
2311 AAAGCCGTCG CATGCTGTAT TGCTCACCAG GTAAATGTCG CTAATGTTT CCAACGCGAG AAGGTGTTGA
2381 GCGCGGAGCT GAGTACGCTG ACAACATGGG TATGCCCAAT TGCCCCATGT TGGGAGGACG AAAATGGTGA
2451 CAAGACAGAT GGCCAGAAAT ACACCAACAG CACGCATGAT GTCTACTGGG GATTATTCTT TTAGTGCGGG
2521 GGAATACACG GCTTTTAATA CGATTGAGGG CGTCTCCTAA CAAGTTACAT CACTCCTGCC CTTCCTCACC
2591 CTAGCTTCCA TCACCTCCTT CATCTCCGTC TATGCCCTCA TCACCTCCG TCACCTCCG CCGCAGCCCC
2661 GGTGGAACCC AGGGAGGCAA ATCTACTCCA TCGTCAAAGC TGCACACAGT CACCTGATA TTGCAGGTAG
2731 GAGCGGGCTT GTGCATAACA AGGTCTCTAA TCGCATCCTT CAAAACCTCA GCAATATATG GAGTTGTGTA
2801 AAAGACCATC AAATAACAGA CAATGGACTC CTTAGCGGG CCAGGTTGTG GCGCGGGTCC AGGGGCGTAA
2871 CCAAAGGGGA GACGACTCAA TGGTGTAAAG CGACATTGTG GAATAGCAAG GGCAGTTCCCT CGCCTTAGGT
2941 TGTAAGGGGA GGTCTTACTA CCTCCATATA CGAACACACC GGCAGCCCAA GTTCTCTCGT CGGTAGTCTC
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3151 CAGTGTCTGG GCCTCTCTCT GGGTCATCTG CCGGGCCCTG CTCTATCGCT CCCGGGGGCA CTGACGGCTC
3221 ACCATCTGGG CCACCTTCTT GGTGGTATTC AAAATAATCG GCTTCCCTCA CAGGGTGGAA AGATGGCCTT
3291 CTACCTGGAG GGGGCTGCG CGGTGGAGAC CCGGATGATG ATGACTGACT ACTGGGACTC CTGGGCTCT
3361 TTTCTCCACG TCCACGACCT CTCCCCTGG CTCTTTTACG ACTTCCCCC CTGGCTCTTT CACGTCTCT
3431 ACCCGGGGCG CTTCCACTAC CTCCCTGACC CCGGCTCCA CTACCTCTC GACCCCGGCC TCCACTGCC
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3711 CCTGCCCCCT CTGCCCCCTC TGCTCTGCTC CCTCTGCCCC TCCTGCCCCC TGCCCCCTCT GCTCTGCCCC
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3851 TGCTCTGCTC CCTCTGCCCC TCCTGCCCCC CTCTGCCCCC GCCCCTCTC CTGCTCTCTG CCCCCTCTG
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4061 TCCTGCTCCT GCCCCCTCTG CCCCCTCTG CCTGCTCTG CCCCCTCTC TGCTCTGCTC CCTCTGCTC
4131 CCTGCCCCCT CTGCCCCCTC TGCCCCCTCT CCTGCTCTG CCCCCTCTC TGCTCTGCTC CCTCTGCTC
4201 CTGCCCCCTC CGCTCTGCTC CTGCTCTCTG TTTCCACGTT GGTCCCTTTG CAGCCAATGC AACTTGGAGC
4271 TTTTGGGGT CTCGGGACAC CATCTCTATG TTTTGGCCCT GATCCTGAGC GATCCTGAGC TCTGCTCTT
4341 CCGCTCTCTC GTCCTCGTCC TCTTCCCCGT CCTCGTCCAT GGTATACACC CCCTCTCTT TGAGGTCCAC
4411 TGCCCGCCGA GCCTTCTGTT CCAGATGTGT CTCCCCTCTC TCCTAGGCCA TTTCCAGGTC CTGACTCTGG
4481 CCCCTCGTCA GACATGATTC ACACATAAAG AGCCCCCCCA CCCTCATCCC CTTCATGGTC GCTGTACAGC
4551 CAGGAGTGC AGACTCCTGC CCCCTCCAAC AGCCCCCCCA CCCTCATCCC CTTCATGGTC GCTGTACAGC
4621 AGATCCAGGT CTGAAAATTC CCCATCTCTC GAACCATCTC CGTCTCATC ACCAATTAAT CAGTGAATA
4691 AAAACTCCCC CTGAACATTC TCAAGATTG GTCCCTGAGC CTCAAGCCAG GCCTCAAATT CCTCGTCCC
4761 CTTTTTGTCT GACGGTAGGG ATGGGGATTC TCGGGACCCC TCCTCTCTCT CTTCAGGTC ACCAGACAGA
4831 GATGCTACTG GGGCAACGGA AGAAAAGCTG GGTGCGCCCT GTGAGGATCA GCTTATCGAT GATAAGCTGT

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100509002 "011302

4901 CAAACATGAG AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA TGTCATGATA  
4971 ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTATTATTT  
5041 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA  
5111 AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCTTTT TTGCGGCATT TTGCCCTTCT  
5181 GTTTTTGCTG ACCCAGAAAC GCTGGTGAAA GTAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT  
5251 ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT  
5321 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTGACG CCGGGCAAGA GCAACTCGGT  
5391 CGCCGCATAC ACTATTCTCA GAATGACTTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT  
5461 GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT  
5531 GACAACATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT  
5601 GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACAGACCCGT TACTCTAGCT TCCCGGCAAC AATTAATAGA  
5671 TGGCAACAAC GTTGCAGAAA CTATTAACCT GCGAACCTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA  
5741 CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT  
5811 GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAAGCCT  
5881 CCGGTATCGT AGTTATCTAC ACGACGGGGA GTACAGGCAAC TATGGATGAA CGAAATAGAG AGATCGCTGA  
5951 GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTGAGAC CAAGTTTACT CATATATACT TTAGATTGAT  
6021 TTAAAACTCT ATTTTAAATT TAAAAGGATC TAGGTGAAGA TCCTTTTGA AAAGGATCTT CTGAGATCC  
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6161 TTTTTTCTG CCGGTAATCT GCTGCTTGA AAAAAAAG CCACCGCTAC CAGCGGTGGT TGTGTTGCGG  
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6511 CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCGCCGAG GGAAGAAAGC  
6581 GGACAGGTAT CCGGTAAGCG GCAGGGTCCG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC  
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6721 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACAGCGGCTT TTTACGGTTC CTGCGCTTTT GTGCGCGCGC  
6791 GTGCGGCTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT GGTGTGCGCA TTCACAGTTC  
6861 TCCGCAAGAA TTGATTGGCT CCAATTCCTG GAGTGGTGAA TCCGTTAGCG AGGCCATCCA GCCTCGCGTC  
6931 GAAGTATGCA AAGCATGCAT CTCATATTAGT CAGCAACCAG GTGTGGAAG TCCCGAGGCT CCCAGCAGG  
7001 CAGAAGTATG CAAAGCATGC ATCTCAATTA GTGAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG  
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7281 ACCGGTGCCG CACCATATCC CTGACCCACG CCCCTGACCC CTCACAAGGA GACGACCTTC CATGACCGAG  
7351 TACAAGCCGA GAGTGGGCTG CGCCACCCG ACAGCGCTCC CCGGGGCCGT ACGCACCCCT CGCGCCGCGT  
7421 TCGCCGACTA CCGCCGACG CGCCACCCG TCGACCCGGA CCGCCACATC GAACGCGTCA CCGAGCTGCA  
7491 AGAAGTCTTC CTCACGCGCG TCGGGCTCGA CATCGGCAAG GTGTGGGTCG CGGACGACGG CGCCGCGGTG  
7561 GCGGTCTGTT CACAGCCGGA GAGCGTCCGA GCGGGGGCGG TGTTCGCGCA GATCGGCCCG GCATCGGCCG  
7631 AGTTGAGCGG TTCCCGGCTG GCGCGCAGC AACAGATGGA AGGCTCCTG GCGCCGACG GGGCCAAGGA  
7701 GCGCGCGTGG TTCTTGCCCA CCGTCCGCGT CTCGCCCGAC CACCAGGGGA AGGGTCTGGG CAGCGCCGTC  
7771 GTGCTCCCCG GAGTGGAGGC CTCGGCTTCA CCGTACCCGC CGACGTCGAG TGCCCGAAGG ACCGCGCGAC  
7841 ACCTCCCCCT CTACGAGCGG CTCGGCTTCA CCGTACCCGC CGACGTCGAG TGCCCGAAGG ACCGCGCGAC  
7911 CTGGTGATG ACCCGCAAGC CCGGTGCTG ACGCCCGCCC CACGACCCGC AGCGCCCGAC CGAAAGGAGC  
7981 GCACACCAAT GTCCGACGGC GCGCCACGGG TCCAGGGGGG GTCGACCTCG AAACCTTGTTT ATTCGAGCTT  
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8121 TTGTGGTTTG TCCAAACTCA TCAATGTATC TTATCATGTC TGGATCGATC CGAACCCCTT CCTCGACCA  
8191 TTCTCATGTT TCAAGCTTCA TCATCGAGA TCCGGGCAAC GTTGTGTCAT TGCTGCAGGC TGCATGCTGG  
8261 TAGGTATGGA AGATCTATAC ATTGAATCAA TATTGGCAAT TAGCCATATT AGTCATTGGT TATATAGCAT  
8331 AAATCAATAT TGGCTATTGG CCAATGTCAT CGTTGTATCT ATATCATAAT ATGTACATTT ATATTGGCTC  
8401 ATGTCCAATA TGACCGCCAT GTTGACATTG ATTTAGTACT AGTTATTAAT AGTAATCAAT TACGGGTCA  
8471 TTAGTTCATA GCGCATATAT GGAGTTCGCG GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC  
8541 CCAACGACCC CCGCCCATTT ACCTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA  
8611 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTTGGCCA TTGGCAGTAC ATCAAGTGTA ATCATGCGCA  
8681 AGTCCGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC ATGACCTTAC  
8751 GGGAGTTTTC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA  
8821 GTACACCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCAACCCAT TGACGTCAAT  
8891 GGGAGTTTGT TTTGGCACCA AAATCAACGG GACTTTCCAA AATGTCGTAA TAACCCCGCC CCGTTGACGC  
8961 AAATGGGCGG TAGGCGTGTA CCGTGGGAGG TCTATATAAG CAGAGCTCGT TTAGTGAACC GTCAGATCTC  
9031 TAGAAGCTGG GTACCGGGAT CCAGCAGCTG GGTTCGAGGT GCTAGCGGGA GGGGGTGGAT GTGGGATCGA  
9101 AGGTGCGAAG CTTACTCACA CATGCCACC GTGCCAGCA CCTGAAGCCG AGGGGGCACC GTCAGTCTTC  
9171 CTCTTCCCCC CAAAACCCAA GGACACCCCT ATGATCTCCC GGACCCCTGA GGTACATGCG GTGTGTTGG  
9241 ACGTGAGCCA CGAAGACCTT GAGGTCAAGT TCAACTGTTA CGTGGACGGC GTGGAGGTGC ATAAATGCCAA  
9311 GACAAAGCCG CCGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT CTGCACCCAG  
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9451 CCATCTCCAA AGCCAAAGGG CAGCCCGGAG AACCAAGGT GTACACCTG CCCCACCTCC GCGATGAGCT  
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9661 TCCTCTACAG CAAGCTCACC GTGGACAAGA GCAGGTGGCA TCCCTGTCTC CCGGTAAATG ACTCGAGGCC  
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9801 CGAACAAAAA CTCATCTCAG AAGAGGATCT GAATAGCGCC GTGACCATC ATCATCATCA TCATTGAGTT  
9871 TNAACGATCC AGACATGATA AGATACATTG ATAGTTTGG GTCTTTATTT GTAACCATTA TAAGCTGCAA TAAACAAGTT  
9941 ATGCTTTATT TGTGAAATTT GTGATGCTAT TGCTTTATTT GAGGTTTGGT GAGGTTTGGT AAAGCAAGTA  
10011 AACAACAACA ATTGCAATCA TTTTATGTTT CAGGTTTCAG GGGAGGTGGG GAGGTTTGGT AAAGCAAGTA  
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10151 ACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG TCTGTAAGCG GATGCCGGGA GCAGACAAGC  
10221 CCGTCAGGGC GCGTCAGCGG GTGTTGGCGG GTGTCGGGGC GCAGCATGTA CCGGTGCGACT CTAGA

10050902 "01.1902"

284:

5'LT• : (SEQ ID NO:284)

5'-CTT GGT GCC GCA GGA TCA G-3'

285:

3'LT• : (SEQ ID NO:285)

5'-CAG ATG GCT GTC ACC CCA C-3'

286:

5'LT• long-*Nhe*I: (SEQ ID NO:286)

5'-GCC CGC TAG CCT GCG GTG GTC AGG ATC AGG GAC GTC G-3'

287:

5'LT• short-*Nhe*I: (SEQ ID NO:287)

5'-GCC CGC TAG CCT GCG GTG GTT CTC CAG CTG CGG ATT C -3'

288:

3'LT• stop-*Not*I: (SEQ ID NO:288)

5'-CAA TGA CTG CGG CCG CTT ACC CCA CCA TCA CCG -3'

289:

GST-EK-C-LT•<sub>49-306</sub>: SEQ ID NO:289

APLVMSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ  
SMAIIRYIADKHNMLGGCPKERAIEISMLEGAVLDIRYGVSRISYKDFETLKVDFLSKLPEMLKMFEDRLCH  
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGWQATF  
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIIGSGAQAQKRLDDSKPSCILPSPSSL  
SETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDGPVQQLPKGEPETDLNPEL  
PAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVVYLYCHVGYRGRTPPAGRSRARS  
LTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVVYNISHPDMV  
DYRRGKTFFGAVMVG

290:

GST-EK-C-LT•<sub>126-306</sub>: SEQ ID NO:290

20870"2060500T

APLVMSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ  
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KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGWQATF  
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGPVQQLPKGEPETDLNPELPAHLIGA  
WMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSRTLRSALY  
RAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGKT  
FFGAVMVG

291:

his-myc-EK-C-LT• 49-306: SEQ ID NO:291

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQ  
AQKRLDDSKPSCILPSPSSLSETPDPRHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDGPV  
QQLPKGEPETDLNPELPAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGY  
RGRTPPAGRSRARSRTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSG  
ERVYVNISHPDMVDYRRGKTFFGAVMVG

292:

his-myc-EK-C-LT• 126-306: SEQ ID NO:292

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGPVQQLP  
KGEPETDLNPELPAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRT  
PPAGRSRARSRTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVY  
VNISHPDMVDYRRGKTFFGAVMVG

293:

primerMCS-1F

5'-TAT GGA TCC GGC TAG CGC TCG AGG GTT TAA ACG GCG GCC GCA T-3' (SEQ ID NO:293)

294:

primerMCS-1R

5'-TCG AAT GCG GCC GCC GTT TAA ACC CTC GAG CGC TAG CCG GAT CCA-3' (SEQ ID NO:294)

295:

Bamhis6-EK-Nhe-F

5'-GAT CCA CAC CAC CAC CAC CAC GGT TCT GGT GAC GAC GAT GAC AAA GCG CTA GCC C-3'  
(SEQ ID NO:295)

20250502 10:50:02

296:

Bamhis6-EK-Nhe-R

5'-TCG AGG GCT AGC GCT TTG TCA TCG TCG TCA CCA GAA CCG TGG TGG TGG TGG TGG TGT G-3'  
(SEQ ID NO:296)

297:

oligo1F-C-glycine-linker

5'-TCG AGG GTG GTG GTG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:297)

298:

oligo1R-C-glycine-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCA CCA CCA CCC-3' (SEQ ID NO:298)

299:

oligo1F-C-gamma1-linker

5'-TCG AGG ATA AAA CCC ACA CCT CTC CGC CGT GTG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:299)

300:

oligo1R-C-gamma1-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCA CAC GGC GGA GAG GTG TGG GTT TTA TCC-3' (SEQ ID NO:300)

301:

oligo1FA-C-gamma3-linker

5'-TCG AGC CGA AAC CGT CTA CCC CGC CGG GTT CTT CTG-3' (SEQ ID NO:301)

302:

oligo1RA-C-gamma3-linker

5'-CAC CAC CAG AAG AAC CCG GCG GGG TAG ACG GTT TCG GC-3' (SEQ ID NO:302)

2025-09-20 10:05:00

303:

oligo2FB-C-gamma3-linker

5'-GTG GTG CTC CGG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:303)

304:

oligo2RB-C-gamma3-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCC GGA G-3' (SEQ ID NO:304)

305:

rMIF-F

5'-GGA ATT CCA TAT GCC TAT GTT CAT CGT GAA CAC-3' (SEQ ID NO:305)

306:

rMIF-Xho-R

5'-CCC GCT CGA GAG CGA AGG TGG AAC CGT TC-3' (SEQ ID NO:306)

307:

rMIF-C1:

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ  
NRNYSKLLCGLLSDR LHISPDRVYINYYDMNAANVGWNGSTFALEGGGGGCG (SEQ ID NO:307)

308:

rMIF-C2

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ  
NRNYSKLLCGLLSDR LHISPDRVYINYYDMNAANVGWNGSTFALEDKTHTSPPCG (SEQ ID NO:308)

309:

rMIF-C3

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ  
NRNYSKLLCGLLSDR LHISPDRVYINYYDMNAANVGWNGSTFALEPKPSTPPGSSGGAPGGCG (SEQ ID  
NO:309)

10050902-011302

310:

met-human-MIF-C1

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEGGGGGCG

311:

human-MIF-C1 (SEQ ID NO:311)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEGGGGGCG

312:

met-human-MIF-C2 (SEQ ID NO:312)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEDKTHTSPPCG

313:

human-MIF-C2 (SEQ ID NO:313)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEDKTHTSPPCG

314:

met-human-MIF-C3 (SEQ ID NO:314)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLCGLLAERLRISPDRVYINYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

315:

human-MIF-C3 (SEQ ID NO:315)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS  
LHSIGKIGGA QNRSYSKLLCGLLAERLRISPDRVYINYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

316:

RANKL-UP:

5'CTGCCAGGGGCCCCGGGTGCGGCGGTGGCCATCATCACCACCATCACCAGCGCTTCTCAGGAG-3'

317:

RANKL-DOWN :

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5'-CCGCTCGAGTTAGTCTATGTCCTGAACTTTGAAAAG-3'

318 and 319:

Protein sequence of GST-PS-C-RANKL (SEQ ID NO:318; capital letters)

cDNA sequence of GST-PS-C-RANKL (SEQ ID NO:319; small letters)

1 M S P I L G Y W K I K G L V Q P T R L L L E Y L E  
1 atgtcccctatactaggttatttgaaaattaagggccttggtgcaaccactcgacttcttttggaatatcttgaa  
26 E K Y E E H L Y E R D E G D K W R N K K F E L G L  
76 gaaaaatatgaagagcatttgtatgagcgcatgaaggatgataaatggcgaaacaaaaagtttggaattgggtttg  
51 E F P N L P Y Y I D G D V K L T Q S M A I I R Y I  
151 gagtttcccaatcttcttattatattgatggtgatgttaaattaacacagtcctatggccatcatacgttatata  
76 A D K H N M L G G C P K E R A E I S M L E G A V L  
226 gctgacaagcacaacatgttggtggttgccaaaagagcgtgcagagatttcaatgcttgaaggagcggttttg  
101 D I R Y G V S R I A Y S K D F E T L K V D F L S K  
301 gatattagatacgggtgtttcgagaattgcatatagtaaagactttgaaactctcaaagttgattttcttagcaag  
126 L P E M L K M F E D R L C H K T Y L N G D H V T H  
376 ctacctgaaatgctgaaaatgttcgaagatcggttatgtcataaaacatatattaaatggtgatcatgtaacccat  
151 P D F M L Y D A L D V V L Y M D P M C L D A F P K  
451 cctgacttcatgttgatgacgctcttgatgttggtttttatatacatggacccaatgtgcctggatgcgttcccaaaa  
176 L V C F K K R I E A I P Q I D K Y L K S S K Y I A  
526 ttagtgtgttttaaaaaacgtattgaagctatcccaaaattgataagtaacttgaatccagcaagtatatagca  
201 W P L Q G W Q A T F G G G D H P P K S D L E V L F  
601 tggccttttgcaagggttgcaagccacgtttggtggtggcgaccatcctccaaaatcggatctggaagttctgttc  
226 Q G P G C G G G H H H H Q R F S G A P A M M E  
676 caggggccccgggtgccccgggtgccccatcatcaccaccatcaccagcgcttctcaggagctccagctatgatggaa  
251 G S W L D V A Q R G K P E A Q P F A H L T I N A A  
751 GGCTCATGGTGGATGTGGCCCGAGGCAAGCCTGAGGCCAGCCATTGACACCTCACCATCAATGCTGCC  
276 S I P S G S H K V T L S S W Y H D R G W A K I S N  
826 AGCATCCCATCGGTTCCCAAAAGTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAAC  
301 M T L S N G K L R V N Q D G F Y Y L Y A N I C F R  
901 ATGACGTTAAGCAACGGAAAACCTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTGCTTTTCGG  
326 H H E T S G S V P T D Y L Q L M V Y V V K T S I K  
976 CATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCGTTAAACAGCATCAAA  
351 I P S S H N L M K G G S T K N W S G N S E F H F Y  
1051 ATCCCAAGTTCTCATAACCTGATGAAAGGAGGAGCACGAAAACTGGTCGGGCAATTCTGAATTCCACTTTTAT  
376 S I N V G G F F K L R A G E E I S I Q V S N P S L  
1126 TCCATAAATGTTGGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATAGCATTGAGGTGTCCAACCTTCCCTG  
401 L D P D Q D A T Y F G A F K V Q D I D \*  
1201 CTGGATCCGATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTCAGGACATAGACTAACTCGAGCGG

320:

Human-C-RANKL

CGGGQHIRAEKAMVDGSLDLAKRSKLEAQPFHAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLI  
VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFK  
LRSGEEISIEVSNPSLLDPQDATYFGAFKVRDID

321:

Primer 5'PrP-BamHI

5'-CGG GAT CCC ACC ATG GTG GGG GGC CTT GG -3' (SEQ ID NO:321)

322:

Primer 3'PrP-NheI

5'-CTA GCT AGC CTG GAT CTT CTC CCG -3' (SEQ ID NO:322)

323:

Protein sequence of mPrP<sub>t</sub>-EK-Fc\*

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT  
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDKLTHTCPPCPAPEA  
EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS  
VLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS  
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG  
K

324:

mPrP<sub>t</sub>

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT  
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDK

325:

human resistin-C-Xa: (SEQ ID NO:325)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL  
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG  
IEGR

326:

human resistin-C-EK: (SEQ ID NO:326)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL  
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG  
DDDDK

327:

human resistin-C: (SEQ ID NO:327)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL  
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG

328:

10050902-01302

mouse C-IL-13-F: (SEQ ID NO:328)

ADPGCGGGGGLAGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSL TNISNCN  
AIYRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPFLEVLAIEGR

329:

mouse C-IL-13-S: (SEQ ID NO:329)

LACGGGGGGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSL TNISNCNAI  
YRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

330:

human C-IL-13-F: (SEQ ID NO:330)

ADPGCGGGGGLAGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCS  
AIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKCLFREGRFNLEVLAIEGR

331:

human C-IL-13-S: (SEQ ID NO:331)

LACGGGGGGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR  
MLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKCLFREGRFN

332:

mouse C-IL-5-E: (SEQ ID NO:332)

ALVCGGPKPSTPPGSSGGAPASMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQG  
LDILKNQTVRGGTVEMLFQNL SLIKKYIDRQKEKCGEERRRTRQFLDY LQEFLGVMSTEWAMEG

333:

mouse C-IL-5-F: (SEQ ID NO:333)

ADPGCGGGGGLAMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVR  
GGTVEMLFQNL SLIKKYIDRQKEKCGEERRRTRQFLDY LQEFLGVMSTEWAMEGLEVLAIEGR

334:

mouse C-IL-5-S: (SEQ ID NO:334)

LACGGGGGMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRGG  
TVEMLFQNL SLIKKYIDRQKEKCGEERRRTRQFLDY LQEFLGVMSTEWAMEG

335:

human C-IL-5-E: (SEQ ID NO:335)

ALVCGGPKPSTPPGSSGGAPASIPTEIPTALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGI  
GTLESQTVQGGTVERLFKNL SLIKKYIDGQKKCGEERRRVNQFLDY LQEFLGVMNTEW IIES

336:

human C-IL-5-F: (SEQ ID NO:336)

10050902 "0150E

ADPGCGGGGGLAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG  
GTVERLFKNLSLIKYYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES LEVLAIEGR

337:

human C-IL-5-S: (SEQ ID NO:337)

LACGGGGGIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGT  
VERLFKNLSLIKYYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

338:

primer NheIL13-F: (SEQ ID NO:338)

CTAGCTAGCCGGGCGCGGTGCCAAGATC

339:

primer XhoIL13-R: (SEQ ID NO:339)

TTTCTCGAGGAAGGGGCGGTGGCGAA

340:

primer Spelinker3-F1: (SEQ ID NO:340)

CCCCGCCGGGTTCTTCTGGCGGTGCTCCGGCTAGCATGGAGATTCCCATGAGCAC

341:

Primer SpeNlinker3-F2: (SEQ ID NO:341)

TTTTACTAGTTGGTTGCGGCGGCCCCGAAACCGAGCACCCCGCCGGGTTCTTC

342:

Primer IL5StopXho-R: (SEQ ID NO:342)

TTTTGCGGCCGCGTTTAAACTCGAGTTATTAGCCTTCCATTGCCCACTC

343:

Primer BamH1-FLK1-F: (SEQ ID NO:343)

CGCGGATCCATTCATCGCCTCTGTC

344:

Primer Nhe1-FLK1-B: (SEQ ID NO:344)

CTAGCTAGCTTTGTGTGAACTCGGAC

345:

mVEGFR-2 (2-3) fragment: (SEQ ID NO:345)

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PFIAS VSDQHGIYVI TENKNKTVVI PCRGSISNLN VSLCARYPEK RFVPDGNRIS WDSEIGFTLP  
SYMISYAGMV FCEAKINDET YQSIMYIVVV VGYRIYDVIL SPPHEIELSA GEKLVNLCTA  
RTELNVGLDF TWHSPPSKSH HKKIVNRDVK PFPGTVAKMF LSTLTIESVT KSDQGEYTCV  
ASSGRMIKRN RTFVRVHTKP

346

human C-LT• 49-306 : (SEQ ID NO:346)

LACGGQDQGRRVEKIIGSGAQAQKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSR  
EASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSP  
THGLALPDQGVYYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIG  
YGSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

347

human C-LT• 126-306 : (SEQ ID NO:347)

LACGGSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPHGL  
ALPDQGVYYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYSL  
WYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

348

Modified human prion protein fragment: (SEQ ID NO:348)

VGGLGGYMLGSAMSRPIHFGSDYEDRYRENMHRYPNQVYYRPMDE  
YSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQRESQAYYQ  
RGRLAGGGGCG

349

Modified bovine prion protein fragment: (SEQ ID NO:349)

VGGLGGYMLGSAMSRPLIHFGSDYEDRYRENMHRYPNQVYYRPVDQ  
YSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ  
RGRLAGGGGCG

350

Modified sheep prion protein fragment: (SEQ ID NO:350)

VGGLGGYMLGSAMSRPLIHFGNDYEDRYRENMYRYPNQVYYRPVDR  
YSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQ  
RGRLAGGGGCG

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